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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:03:14 ; Search time 39 Seconds
(without alignments)
2239.361 Million cell updates/sec

Title: US-09-524-531C-15

Perfect score: 1637
Sequence: 1 MALRRPRLRLCARLPDFL.....VNYIRDEGDFRHKSSFVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1637	100.0	310	9	US-09-909-320-423
2	1637	100.0	310	9	US-09-909-088B-423
3	1637	100.0	310	9	US-09-905-291A-423
4	1637	100.0	310	9	US-09-902-853-423
5	1637	100.0	310	9	US-09-907-824-423
6	1637	100.0	310	9	US-09-907-841-423
7	1637	100.0	310	10	US-09-904-011-423
8	1637	100.0	310	10	US-09-906-742-423
9	1637	100.0	310	10	US-09-906-838-423
10	1637	100.0	310	10	US-09-907-613-423
11	1637	100.0	310	10	US-09-907-942-423
12	1637	100.0	310	10	US-09-904-859-423
13	1637	100.0	310	10	US-09-909-204-423
14	1637	100.0	310	10	US-09-904-820-423
15	1637	100.0	310	10	US-09-904-786-423

16	1637	100.0	310	10	US-09-906-646-423	Sequence 423, App
17	1637	100.0	310	10	US-09-906-700-423	Sequence 423, App
18	1637	100.0	310	10	US-09-903-786-423	Sequence 423, App
19	1637	100.0	310	10	US-09-902-903-423	Sequence 423, App
20	1637	100.0	310	10	US-09-903-749A-423	Sequence 423, App
21	1637	100.0	310	10	US-09-904-119-423	Sequence 423, App
22	1637	100.0	310	10	US-09-904-956-423	Sequence 423, App
23	1637	100.0	310	10	US-09-902-736-423	Sequence 423, App
24	1637	100.0	310	10	US-09-907-794-423	Sequence 423, App
25	1637	100.0	310	10	US-09-903-943-423	Sequence 423, App
26	1637	100.0	310	10	US-09-904-462-423	Sequence 423, App
27	1637	100.0	310	10	US-09-907-925-423	Sequence 423, App
28	1637	100.0	310	10	US-09-902-620-423	Sequence 423, App
29	1637	100.0	310	10	US-09-903-520-423	Sequence 423, App
30	1637	100.0	310	10	US-09-905-056-423	Sequence 423, App
31	1637	100.0	310	10	US-09-909-064-423	Sequence 423, App
32	1637	100.0	310	10	US-09-904-553-423	Sequence 423, App
33	1637	100.0	310	10	US-09-905-381-423	Sequence 423, App
34	1637	100.0	310	10	US-09-905-088-423	Sequence 423, App
35	1637	100.0	310	10	US-09-907-575-423	Sequence 423, App
36	1637	100.0	310	10	US-09-902-759-423	Sequence 423, App
37	1637	100.0	310	10	US-09-902-759-423	Sequence 423, App
38	1637	100.0	310	10	US-09-902-634-423	Sequence 423, App
39	1637	100.0	310	10	US-09-902-713-423	Sequence 423, App
40	1637	100.0	310	10	US-09-907-979-423	Sequence 423, App
41	1637	100.0	310	10	US-09-902-615-423	Sequence 423, App
42	1637	100.0	310	10	US-09-903-925-423	Sequence 423, App
43	1637	100.0	310	10	US-09-906-760A-423	Sequence 423, App
44	1637	100.0	310	10	US-09-903-823-423	Sequence 423, App
45	1637	100.0	310	10	US-09-907-652-423	Sequence 423, App

ALIGNMENTS

RESULT 1

US-09-909-320-423

; Sequence 423, Application US/090909320

; Patent No. US20020132240A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Raton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas P.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/909,320

; CURRENT FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien

US-09-909-088B-423

Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRPPRLRLCARLPDPLLLFRGCLIGAVNLKSSNTPVQEFSEVLSCLITDSQT 60
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DB 61 SDPRLWKIODEQTYVFFDNKIQDLAGRAEILGKTSKIWNVTRDSALYRCVWAR 120
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DB 121 NDRKEIDEIVLTQVKPVPVCRVPRKAVPVGKMATLHCQSEGHPRPHYWYNDVPL 180
QY 181 PTDSRANPRNSSPHLSETGLVFTAVHKDDSGQYCIASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRNSSPHLSETGLVFTAVHKDDSGQYCIASNDAGSARCEQMEVYDL 240
QY 241 NTGGIIGVVLAVLALITGLICCAVRRGYFNNKQDGESYKNPKGPGVNYRTDREG 300
DB 241 NTGGIIGVVLAVLALITGLICCAVRRGYFNNKQDGESYKNPKGPGVNYRTDREG 300
QY 301 DFRHKSFFVI 310
DB 301 DFRHKSFFVI 310

RESULT 2

US-09-909-088B-423
Sequence 423, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.

Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MALRRPRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
QY 61 SDPRIEWKIKQDQTTVPFDNKIQGLAGRAEILGKTSKINWVTRDSALYRCEVVAR 120
DB 61 SDPRIEWKIKQDQTTVPFDNKIQGLAGRAEILGKTSKINWVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGMATLHCQESGHPHPRPHYSWRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGMATLHCQESGHPHPRPHYSWRNDVPL 180
QY 181 PTDSRANPRFNSFHLNSETGLVPTAVHKDQSGQYCIASNDAGSARCEQEVEYDL 240
DB 181 PTDSRANPRFNSFHLNSETGLVPTAVHKDQSGQYCIASNDAGSARCEQEVEYDL 240
QY 241 NIGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQDGSYKPNPKDGVNVRTDEEG 300
DB 241 NIGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQDGSYKPNPKDGVNVRTDEEG 300
QY 301 DFRHKSFSVI 310
DB 301 DFRHKSFSVI 310

RESULT 3

US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-423
Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134; Indels 0; Gaps 0;
Matches 310; Conservative 0; Mismatches 0;
QY 1 MALRRPRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
DB 1 MALRRPRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
QY 61 SDPRIEWKIKQDQTTVPFDNKIQGLAGRAEILGKTSKINWVTRDSALYRCEVVAR 120
DB 61 SDPRIEWKIKQDQTTVPFDNKIQGLAGRAEILGKTSKINWVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGMATLHCQESGHPHPRPHYSWRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGMATLHCQESGHPHPRPHYSWRNDVPL 180
QY 181 PTDSRANPRFNSFHLNSETGLVPTAVHKDQSGQYCIASNDAGSARCEQEVEYDL 240
DB 181 PTDSRANPRFNSFHLNSETGLVPTAVHKDQSGQYCIASNDAGSARCEQEVEYDL 240
QY 241 NIGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQDGSYKPNPKDGVNVRTDEEG 300
DB 241 NIGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQDGSYKPNPKDGVNVRTDEEG 300
QY 301 DFRHKSFSVI 310
DB 301 DFRHKSFSVI 310
RESULT 4
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-824-423

Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPRLRLCARLPDFFLLLRGCLIGAVNLKSSNRTVPVQEFBSVELSCIITDSQT 60
Db 1 MALRRPRLRLCARLPDFFLLLRGCLIGAVNLKSSNRTVPVQEFBSVELSCIITDSQT 60

Qy 61 SDPRIWKKTODEQTTVFFDNKIQDLAGRAEILGKTSLSKIWNVTRDSALYRCEVVAR 120
Db 61 SDPRIWKKTODEQTTVFFDNKIQDLAGRAEILGKTSLSKIWNVTRDSALYRCEVVAR 120

Qy 121 NDRKEIDBEIVELTVQVKPVPFCVCRKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDBEIVELTVQVKPVPFCVCRKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180

Qy 181 PTDSRANPRFNSSFLHNSGTGLVFTAVHKDDSGQYYCIASNDAGSARCEQMEYVDL 240
Db 181 PTDSRANPRFNSSFLHNSGTGLVFTAVHKDDSGQYYCIASNDAGSARCEQMEYVDL 240

Qy 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKDGESYKPKDGVNYIRTDSEG 300
Db 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKDGESYKPKDGVNYIRTDSEG 300

Qy 301 DFRHKSFSVI 310
Db 301 DFRHKSFSVI 310

RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.

;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Paoni, Nicholas P.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/907.841
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-841-423

Query Match 100.0%; Score 1637; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPRLRLCARLPDFFLLLRGCLIGAVNLKSSNRTVPVQEFBSVELSCIITDSQT 60
Db 1 MALRRPRLRLCARLPDFFLLLRGCLIGAVNLKSSNRTVPVQEFBSVELSCIITDSQT 60

Qy 61 SDPRIWKKTODEQTTVFFDNKIQDLAGRAEILGKTSLSKIWNVTRDSALYRCEVVAR 120
Db 61 SDPRIWKKTODEQTTVFFDNKIQDLAGRAEILGKTSLSKIWNVTRDSALYRCEVVAR 120

Qy 121 NDRKEIDBEIVELTVQVKPVPFCVCRKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDBEIVELTVQVKPVPFCVCRKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180

Qy 181 PTDSRANPRFNSSFLHNSGTGLVFTAVHKDDSGQYYCIASNDAGSARCEQMEYVDL 240
Db 181 PTDSRANPRFNSSFLHNSGTGLVFTAVHKDDSGQYYCIASNDAGSARCEQMEYVDL 240

Qy 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKDGESYKPKDGVNYIRTDSEG 300
Db 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKDGESYKPKDGVNYIRTDSEG 300

Qy 301 DFRHKSFSVI 310
Db 301 DFRHKSFSVI 310

RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011

Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
PRIORITY FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
SEQUENCE ID NOS: 423
SEQUENCE ID NO 423
LENGTH: 310
TYPE: PPT
ORGANISM: Homo Sapien

US-09-904-011-423
Query Match 100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
DB 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
QY 61 SDPRIEMKKIQDEQTYTTFVFDNKKIQDGLAGRAEILGKTSLKIKWNTRRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDEQTYTTFVFDNKKIQDGLAGRAEILGKTSLKIKWNTRRDSALYRCEVVAR 120
QY 121 NDRKEIDRIVIELTVQVKPVPVCRVPAVPPVKRATLHCQSESGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDRIVIELTVQVKPVPVCRVPAVPPVKRATLHCQSESGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLANSCTGLVPTAVHKDDSGQYCYCIASNDAGSARCEQEMBYIDL 240
DB 181 PTDSRANPRFRNSSPHLANSCTGLVPTAVHKDDSGQYCYCIASNDAGSARCEQEMBYIDL 240
QY 241 NIGGIIGGVLVVLAVLALITLIGICCAVRRGYFINNKQDGSYKNPKGPDGVNYIRTDDEG 300
DB 241 NIGGIIGGVLVVLAVLALITLIGICCAVRRGYFINNKQDGSYKNPKGPDGVNYIRTDDEG 300
QY 301 DFRHKSSPVI 310
DB 301 DFRHKSSPVI 310
RESULT 8
US-09-906-742-423
Sequence 423, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
PRIORITY FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-423

Query Match 100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVOEFSEVLSLIITDSQT 60
Db 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVOEFSEVLSLIITDSQT 60

Qy 61 SDPRIWKIKIQDEQTTVVYFNDKIQGLAGRAEILGKTSLKIMVTRDSALYRCEVVAR 120
Db 61 SDPRIWKIKIQDEQTTVVYFNDKIQGLAGRAEILGKTSLKIMVTRDSALYRCEVVAR 120

Qy 121 NDRKEIDEIVIELTVQKVPVPCRVKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQKVPVPCRVKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPL 180

Qy 181 PTDGRANPRFNSFHLNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEVEVDL 240
Db 181 PTDGRANPRFNSFHLNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEVEVDL 240

Qy 241 NIGGIIGVLVLAVALITIGICCAVARGYFINKQDGSYKPKGPDGVNYIRTDDEG 300
Db 241 NIGGIIGVLVLAVALITIGICCAVARGYFINKQDGSYKPKGPDGVNYIRTDDEG 300

Qy 301 DFRHKSFPVI 310
Db 301 DFRHKSFPVI 310

RESULT 9

US-09-906-838-423
; Sequence 423, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-423

Query Match 100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-942-423

Query Match 100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLCARLPDFLLFRGCLICAVNLKSNRTFVQSPESVLSCLITDSQT 60
DB 1 MALRRPRLCARLPDFLLFRGCLICAVNLKSNRTFVQSPESVLSCLITDSQT 60
QY 61 SDPRIWKIKQDETTVVFDNKIQGLAGRAEILGKTSIKIWNVTRDSALYRCEVVAR 120
DB 61 SDPRIWKIKQDETTVVFDNKIQGLAGRAEILGKTSIKIWNVTRDSALYRCEVVAR 120

QY 121 NDRKEIDRIVIELTVQVXPVTPVCRVPAVPVGRKATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDRIVIELTVQVXPVTPVCRVPAVPVGRKATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCBQEMEVYDL 240
DB 181 PTDSRANPRFRNSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCBQEMEVYDL 240
QY 241 NIGGIIGGLVVLAVLALITLGI CCAYRGGYFIPNNKQDGESYKPKPDGVNVIKRTDESG 300
DB 241 NIGGIIGGLVVLAVLALITLGI CCAYRGGYFIPNNKQDGESYKPKPDGVNVIKRTDESG 300
QY 301 DFRKSSFVI 310
DB 301 DFRKSSFVI 310
RESULT 12
US-09-904-859-423
Sequence 423, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214

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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-423

Query Match      100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
DB 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
QY 61 SDPRIEMKKIQDEQTTTYPFDNKKIQDLAGRAEILGKTSKLIWNVTRDSALYRCVVAR 120
DB 61 SDPRIEMKKIQDEQTTTYPFDNKKIQDLAGRAEILGKTSKLIWNVTRDSALYRCVVAR 120
QY 121 NDRKEIDEIVELTVQVKPVTVCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVELTVQVKPVTVCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSQYYCIAASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSQYYCIAASNDAGSARCEQEMEVYDL 240
QY 241 NIGGIIGVVLVAVLALITLIGICAYRRGYPINNKQGESYKNGKPGDGVNYIRTDREG 300
DB 241 NIGGIIGVVLVAVLALITLIGICAYRRGYPINNKQGESYKNGKPGDGVNYIRTDREG 300
QY 301 DFRHKSSPVI 310
DB 301 DFRHKSSPVI 310
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RESULT 13
US-09-909-204-423
; Sequence 423, Application US/0909204
; Publication No. US2003036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
```

```
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-204-423

Query Match      100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
DB 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
QY 61 SDPRIEMKKIQDEQTTTYPFDNKKIQDLAGRAEILGKTSKLIWNVTRDSALYRCVVAR 120
DB 61 SDPRIEMKKIQDEQTTTYPFDNKKIQDLAGRAEILGKTSKLIWNVTRDSALYRCVVAR 120
QY 121 NDRKEIDEIVELTVQVKPVTVCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVELTVQVKPVTVCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSQYYCIAASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSQYYCIAASNDAGSARCEQEMEVYDL 240
```


APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,786
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-786-423

Query Match 100.0%; Score 1637; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAIRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVOEFESVELSCIITDSQT	60
Db	1	MAIRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVOEFESVELSCIITDSQT	60
Qy	61	SDPRIEWKKIQDEQTTVPFDNKIQGDLGRAEILGKTSKINVTTRDSALYRCEVVAR	120
Db	61	SDPRIEWKKIQDEQTTVPFDNKIQGDLGRAEILGKTSKINVTTRDSALYRCEVVAR	120
Qy	121	NDKREIDEIVIELTVQVKPVPVCRVPRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL	180
Db	121	NDKREIDEIVIELTVQVKPVPVCRVPRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL	180
Qy	181	PTDSRANPRFRNSSFHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEYDL	240
Db	181	PTDSRANPRFRNSSFHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEYDL	240
Qy	241	NIIGGIIGVVLAVLALITLGICAYRGYFINNKQDGESYKNPKPGDGVNVRTDEG	300
Db	241	NIIGGIIGVVLAVLALITLGICAYRGYFINNKQDGESYKNPKPGDGVNVRTDEG	300
Qy	301	DFRKSSFVI 310	
Db	301	DFRKSSFVI 310	

Search completed: June 15, 2004, 11:08:02
Job time : 40 secs

Db 241 AAVLVTLILLGILVPGIFAYSRGHFDRTKGTSSKKVIYSQPS-----ARSEGEF 291

QY 303 RHKSFFVI 310

Db 292 KQTSSFLV 299

RESULT 2

J80099

neural cell adhesion molecule 1 - African clawed frog

N:Alternate names: NCAM 1

C:Species: Xenopus laevis (African clawed frog)

C>Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: J80099

R:Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohara, K.

Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A:Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma

A:Reference number: J80099; MUID:98204770; PMID:9535795

A:Accession: J80099

A:Molecule type: mRNA

A:Residues: 1-725 <KUD>

A:Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227

A:Experimental source: heart

C:Comment: This protein mediates and regulates various cell-cell interactions through bo

C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

F:512-589/Domain: immunoglobulin homology <IMM>

Query Match 11.4%; Score 187; DB 2; Length 725;

Best Local Similarity 28.9%; Pred. No. 1.6e-07;

Matches 61; Conservative 30; Mismatches 84; Indels 36; Gaps 11;

QY 30 GAVNLK-----SSNTPVVOEPESVELSCIITSDPR-IEWK-KIQDEQTTVFFDN 82

Db 105 GTVNLKIYQKLTFFKNAPTQPEFKEGEDAVIICDVSSIPSIITWRHKGKD-----VIFKK 159

QY 83 KIQDLAGRAEILGKTSIKIWNVTRDSALYCE--VVARND--RKEIDIV-IELTVQV 137

Db 160 DV-----RFVVLANNYLQIRIKKTDGTYCEGRILARGEINIKYQIVNVNPTTQA 213

QY 138 KPVTVPVCPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPRFNSFHL 197

Db 214 RQL-----RVNATANKAESVVLSC-DADGFPDPPEISWLKKEGIEDG-----BEKISF 260

QY 198 NSETGLVFTAVHKDSDGQYCIASNDAGSA 228

Db 261 NEDQSEWTHHVEKDDEAFYSCIANNQAGEA 291

RESULT 3

IXLNL

neural cell adhesion molecule long domain form precursor - African clawed frog

N:Alternate names: NCAM-180

C:Contains: neural cell adhesion molecule, short domain form (NCAM-140)

C:Species: Xenopus laevis (African clawed frog)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C:Accession: S09600

R:Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.

Nucleic Acids Res. 17, 10321-10335, 1989

A:Title: Primary structure and developmental expression of a large cytoplasmic domain fo

A:Reference number: S09600; MUID:90098871; PMID:2481269

A:Accession: S09600

A:Molecule type: mRNA

A:Residues: 1-1088 <KKI>

A:Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610

A>Note: the authors translated the codon AAA for residue 970 as Leu

C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C:Comment: Several forms of NCAM are produced by alternative splicing.

C:Genetics:

A:Gene: NCAM

C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <I

F:20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status p

F:20-705/Domain: extracellular #status predicted <EXT>

F:34-95/Domain: immunoglobulin homology <IMM1>

F:129-188/Domain: immunoglobulin homology <IMM2>

F:149-153/Region: heparin binding #status predicted

F:158-162/Region: heparin binding #status predicted

F:225-284/Domain: immunoglobulin homology <IMM3>

F:317-381/Domain: immunoglobulin homology <IMM4>

F:413-475/Domain: immunoglobulin homology <IMM5>

F:512-589/Domain: fibronectin type III repeat homology <FN3A>

F:618-679/Domain: fibronectin type III repeat homology <FN3B>

F:706-723/Domain: transmembrane #status predicted <TM>

F:724-1088/Domain: intracellular #status predicted <INT>

F:41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted

F:219,310,341,417,443,472/Binding site: carbohydrate (Asn) #status predicted

Query Match 11.4%; Score 186; DB 1; Length 1088;

Best Local Similarity 28.9%; Pred. No. 3.2e-07;

Matches 61; Conservative 30; Mismatches 84; Indels 36; Gaps 11;

QY 30 GAVNLK-----SSNTPVVOEPESVELSCIITSDPR-IEWK-KIQDEQTTVFFDN 82

Db 105 GTVNLKIYQKLTFFKNAPTQPEFKEGEDAVIICDVSSIPSIITWRHKGKD-----VIFKK 159

QY 83 KIQDLAGRAEILGKTSIKIWNVTRDSALYCE--VVARND--RKEIDIV-IELTVQV 137

Db 160 DV-----RFVVLANNYLQIRIKKTDGTYCEGRILARGEINIKYQIVNVNPTTQA 213

QY 138 KPVTVPVCPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPRFNSFHL 197

Db 214 RQL-----RVNATANKAESVVLSC-DADGFPDPPEISWLKKEGIEDG-----BEKISF 260

QY 198 NSETGLVFTAVHKDSDGQYCIASNDAGSA 228

Db 261 NEDQSEWTHHVEKDDEAFYSCIANNQAGEA 291

RESULT 4

CS4689

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor

N:Alternate names: MPTP delta type B/C

C:Contains: protein tyrosine phosphatase, receptor type delta, splice form C

C:Species: Mus musculus (house mouse)

C>Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999

C:Accession: CS4689; B54689

R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.

Mol. Cell. Biol. 13, 5513-5523, 1993

A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specializ

A:Reference number: A54689; MUID:93360986; PMID:8355697

A:Accession: CS4689

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1894 <MIZ>

A:Experimental source: brain; splice form B

A>Note: sequence inconsistent with nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)

A:Accession: B54689

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MIZ>

A:Experimental source: brain; splice form C

A>Note: sequence inconsistent with nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester by

F:45-107/Domain: immunoglobulin homology <IMM1>

F:245-299/Domain: immunoglobulin homology <IMM2>

F:317-399/Domain: fibronectin type III repeat homology <FN3A>

F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted

[illegible]

RESULT 8

IJMSNG

neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse

N;Alternate names: NCAM-120

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000

C;Accession: A29673; S00382; A44290

R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec

EMBO J. 6, 907-914, 1987

A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000

A;Reference number: A29673; MUID:87246524; PMID:3595563

A;Accession: A29673

A;Molecule type: mRNA

A;Residues: 1-725 <BA>

A;Cross-references: EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343

R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.

EMBO J. 7, 625-632, 1988

A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM

A;Reference number: S00382; MUID:88283628; PMID:3396534

A;Accession: S00382

A;Molecule type: DNA

A;Residues: 642-656 'D', 658-725 <BA2>

A;Cross-references: EMBL:X07195

R;Rougou, G.; Marshak, D.R.

J. Biol. Chem. 261, 3396-3401, 1986

A;Title: Structural and immunological characterization of the amino-terminal domain of m

A;Reference number: A44290; MUID:86140120; PMID:3512556

A;Accession: A44290

A;Molecule type: protein

A;Residues: 20-36 <ROU>

C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMSNG

C;Genetics:

A;Gene: NCAM

A;Map position: 9

A;Introns: 701/1

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane

P;1-19/Domain: signal sequence #status predicted <SIG>

P;34-98/Domain: immunoglobulin homology <IMM1>

P;132-191/Domain: immunoglobulin homology <IMM2>

P;132-156/Region: heparin binding #status predicted

P;161-165/Region: heparin binding #status predicted

P;228-230/Domain: immunoglobulin homology <IMM3>

P;263-272/Region: NCAM binding #status predicted

P;323-388/Domain: immunoglobulin homology <IMM4>

P;420-482/Domain: immunoglobulin homology <IMM5>

F;519-596/Domain: fibronectin type III repeat homology <FN3A>

F;625-685/Domain: fibronectin type III repeat homology <FN3B>

P;41-96, 139-189, 235-288, 330-386, 427-480/Diulfide bonds: #status predicted

P;222-316, 348, 424, 450, 479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 171.5; DB 1; Length 725;

[illegible]

RESULT 9

IJMSNL

neural cell adhesion molecule 1 precursor, long domain splice form - mouse

N:Alternate names: NCAM-180

N:Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text change 31-Dec-2000

C:Accession: A29673; S00844; S00384; A28281; A44290; S00383

R:Barbats, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontana, E.M.B.O. J. 6, 907-914, 1987

A:Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000

A:Reference number: A29673; MUID:87246524; PMID:3595563

A:Accession: A29673

A:Molecule type: mRNA

A:Residues: 1-548, 'T', 550-571, 'T', 573-574, 'D', 576-588, 'MQR', 593, 'S', 595-599, 'P', 601, 'I'

A:Cross-references: EMBL:Y00051; NID:953342; PIDN:CAA68263.1; PID:G53343

R:Santoni, M.J.; Barbats, D.; Barbats, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; Nucleic Acids Res. 15, 8621-8641, 1987

A:Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neural cell adhesion molecule

A:Reference number: S00844; MUID:88067687; PMID:3684567

A:Accession: S00844

A:Molecule type: mRNA

A:Residues: 529-809, 1077-1115 <S>

A:Cross-references: EMBL:X06328; NID:953322; PIDN:CAA29641.1; PID:G817984

R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.

EMBO J. 7, 625-632, 1988

A:Title: Differential splicing and alternative polyadenylation generates distinct NCAM isoforms

A:Reference number: S00382; MUID:88283628; PMID:3396534

A:Accession: S00384

A:Molecule type: DNA

A:Residues: 642-1115 <BAR>

A:Cross-references: EMBL:X07195

R:Barbats, D.; Vopper, G.; Wille, W.

Nucleic Acids Res. 16, 4217-4225, 1988

A:Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse, is produced by alternative splicing

A:Reference number: A28281; MUID:88247737; PMID:2454455

A:Accession: A28281

A:Molecule type: mRNA

A:Residues: 804-1081 <BAR>

A:Cross-references: EMBL:X07244; NID:953321; PIDN:CAA30230.1; PID:G9297720

R:Rougon, G.; Marshak, D.R.

J. Biol. Chem. 261, 3396-3401, 1986

A:Title: Structural and immunological characterization of the amino-terminal domain of NCAM

A:Reference number: A44290; MUID:86140120; PMID:3512556

A:Accession: A44290

A:Molecule type: protein

A:Residues: 20-36 <ROU>

C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM molecule

C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:ID00100

C:Genetics:

A:Gene: NCAM

A:Map position: 9

A:Introns: 643/3; 701/1; 770/2; 809/2; 1076/2

RESULT 10

1JRTNC

neural cell adhesion molecule short domain form precursor - rat

N;Alternate names: NCAM-140

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999

C;Accession: S00846; B37795; I58136

R;Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.

J. Cell Biol. 105, 2335-2345, 1987

A;Title: Identification of a cDNA clone that contains the complete coding sequence for a

A;Reference number: S00846; MUID:98059265; PMID:3680385

A;Accession: S00846

A;Molecule type: mRNA

A;Residues: 1-858 <SMA>

A;Cross-references: EMBL:X06564

R;Small, S.J.; Akeson, R.

J. Cell Biol. 111, 2089-2096, 1990

A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct

A;Reference number: A37795; MUID:91035620; PMID:1699951

A;Accession: B37795

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 340-381 <SM2>

R;Small, S.J.; Haines, S.L.; Akeson, R.A.

Neuron 1, 1007-1017, 1988

A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev

A;Reference number: I58136; MUID:90166485; PMID:2483093

A;Accession: I58136

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 355-364 <RES>

A;Accession: S12052
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 390-1912 <KRU>
A;Cross-references: GB:X54133; NID:g35789; PIDN:CAR38068.1; PID:g35790
A;Note: the sequence from fig. 5A is inconsistent with that from Fig. 5A in having 568-


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Db 486 TTPPQLQCFNKEVTVSCSATGRE--KPTIQWTKTD-----GSSLPSHVSHRAG 534
Qy 94 ILGKTSIKIWNVTRRDSALYRCEVAVNRDRKEIDIEIVIELTVQVKPVPVCRVKAHPVG 153
Db 535 I-----LSFKVSRSDSGNYTC--IANSPOGEIRATVQLVAVVVFLEPEPTTVYQG 587
Qy 154 KMATLHCQESGHPHPRPHYSWYRNDVPLPTDSRANPRFNSFLHNSGTTLVFTAVHKDD 213
Db 588 HTAMPQCO-AEGDPVPHIQMKDKIL-DPSKLLPRIQ-----IMPNGSLVVDVTTED 639
Qy 214 SGQYVCYCNADG-----SARCEOE-----MEVVDNLNGGIIGGVLV 251
Db 640 SGKYTCIAGNSCNTKREAFIYVVDKPAAESDEGSSHTPYKMIQTIGLSVGAAYVIII 699
Qy 252 VLAVLALITLIGCCAYRRGYFINNKQDGE 280
Db 700 VLGLMP-----YCKRRKAKELKHPGE 723

RESULT 14
IJBONC
N;Alternate names: NCAM-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A32976; B44290; S05402
R;Lipkin, V.M.; Khrantsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki-
FEBS Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and
A;Reference number: A32976; MUID:89378239; PMID:2776887
A;Accession: A32976
A;Molecule type: mRNA
A;Residues: 1-853 <LRP>
A;Cross-references: GB:X16451; NID:g60; PIDN:CAA34470.1; PID:g61
A;Accession: A38778
A;Molecule type: protein
A;Residues: 20-36 <ROU>
A;Note: 23-Glu was also found
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol-
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu-
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si-
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-853/Product: neural cell adhesion molecule, short domain form #status experimental
F;20-719/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-288/Domain: immunoglobulin homology <IMM3>
F;261-270/Region: NCAM binding #status predicted
F;321-396/Domain: immunoglobulin homology <IMM4>
F;428-490/Domain: immunoglobulin homology <IMM5>
F;527-604/Domain: fibronectin type III repeat homology <FN3A>
F;633-693/Domain: fibronectin type III repeat homology <FN3B>
F;720-737/Domain: transmembrane #status predicted <TM>
F;738-853/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F;222,314,346,432,458,487/Binding site: carbohydrate (Asn) #status predicted

Query Match 9.9%; Score 161.5; DB 1; Length 853;
Best Local Similarity 26.0%; Pred No. 2.6e-05;
Matches 60; Conservative 38; Mismatches 88; Indels 45; Gaps 11;
```

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Qy 27 CLIGA-----VNLKSSNR-----TPVQEPESVELSCIITDSQTS-DPRIEMKQIQ 71
Db 96 CVVTAEDGTESEATVNVKIFOKLAFKQKAPTQEFREGBDAVIVCDVSSLPPTIIWK---- 152
Qy 72 DEQTYVYVFNKIQGDLAGRAEILKTSIKIWNVTRRDSALYRCE--VVARNDREIDRI 129
Db 153 -----HKGRDVLKKDV--RFIVLTNNYQLQIRGIKKTDEGYRCEGRILARG--EINPK 202
Qy 130 VIRLTVQVKPVPVCR--VPKAVPVGMKATLHCQESGHPHPRPHYSWYRNDVPLPTDSRAN 187
Db 203 DIQVIVNVPVTVQARQSIVNATNLGQSVTLVC-NAEGFPBPVTSWTKDGEIENE----- 257
Qy 188 PRFNSFLHNSGTTLVFTAVHKDDSGQYVCYCNADNAGSARCEOEVEVY 238
Db 258 ---EDEKYLFDSDSSELTIRKVRNDKDEAVYVCIENKAG-----EQDASIIH 300

RESULT 15
JC2457
vascular cell adhesion protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 08-Oct-1999
C;Accession: JC2457
R;Teang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
Biochem. Biophys. Res. Commun. 201, 805-812, 1994
A;Title: Cloning and expression kinetics of porcine vascular cell adhesion molecule.
A;Reference number: JC2457; MUID:94271236; PMI :7516159
A;Accession: JC2457
A;Molecule type: mRNA
A;Residues: 1-538 <TSA>
A;Cross-references: EMBL:U08351; NID:9474382; IDN:AAA21542.1; PID:9474383
C;Keywords: glycoprotein; transmembrane protein
F;497-517/Domain: transmembrane #status predicted <TM>
F;75,157,271,330,360/Binding site: carbohydrate (Asn) #status predicted

Query Match 9.8%; Score 161; DB 2; Length 538;
Best Local Similarity 29.0%; Pred No. 1.1e-05;
Matches 58; Conservative 23; Mismatches 79; Indels 40; Gaps 8;

Qy 36 SSNRPVQEPESVELSCIITDSQTSDDPRIEM:KIQDEQTYVYVFNKIQGDLAGRAEIL 95
Db 227 SVNPSTSLQEGDSMMWTC--TSEGLPAPQISW:K-----KLDNGDQQLSGNA--- 272
Qy 96 GKTSIKIWNVTRRDSALYRCEV--ARNDRKE:DEIVIELTVQVKP--VTPVCRVKAHP 151
Db 273 ---TLTIIAMRMEDSGIYVCEGVNPNVGTNRKE:-----VELTVQVAPRDTTISVNPSSYLE 324
Qy 152 VGRMATLHCQESGHPHPRPHYSWYRNDVPLPTD:ZANPRFNSFLHNSGTTLVFTAVHK 211
Db 325 EGSSVNWTC-SSDGFPAPKILW-----SKLRDGNLEPLSENTTLTISTFM 370
Qy 212 DSGQYVCYCNADNAGSARCE 231
Db 371 EDSGIYVCEGINQAQINRKE 390

Search completed: June 15, 2004, 11:05:46
Job time : 15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 10:51:49 ; Search time 10 Seconds
(without alignments)

1614.175 Million cell updates/sec

Title: US-09-524-531c-15

Perfect score: 1637

Sequence: 1 MALRRPRLRLCARLPDFL.....VNYRTDEGDPRKKSFSVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	29.8	298	1	JAM2 HUMAN
2	457.5	27.9	300	1	JAM1_MOUSE
3	424	25.9	299	1	JAM1_HUMAN
4	408.5	25.0	298	1	JAM1_BOVIN
5	228.5	14.0	319	1	A33 HUMAN
6	186	11.4	1088	1	NCA1_XENLA
7	177	10.8	1092	1	NCA2_XENLA
8	174	10.6	333	1	ANAL_DROME
9	171.5	10.5	725	1	NCA2_MOUSE
10	171.5	10.5	1115	1	NCA1_MOUSE
11	171	10.4	1377	1	NBO1 RAT
12	170	10.4	837	1	NCA2_HUMAN
13	169.5	10.4	858	1	NCA1 RAT
14	169.5	10.4	1912	1	PTPD_HUMAN
15	169	10.3	837	1	NCA2_MOUSE
16	164.5	10.0	3707	1	PGBM_MOUSE
17	163.5	10.0	1051	1	PTK7_CHICK
18	163	10.0	1091	1	NCA1_CHICK
19	163	10.0	1493	1	NBO1_MOUSE
20	161.5	9.9	853	1	NCA1_BOVIN
21	161	9.8	344	1	NTRI_HUMAN
22	160.5	9.8	761	1	NCA2_HUMAN
23	160.5	9.8	848	1	NCA1_HUMAN
24	159.5	9.7	365	1	CKAR_HUMAN
25	159.5	9.7	6632	1	UN89_CABEL
26	159	9.7	353	1	CEPU_CHICK
27	156	9.5	344	1	NTRI_MOUSE
28	155.5	9.5	1284	1	NCA1_CHICK
29	155	9.5	344	1	NTRI RAT
30	153.5	9.4	1461	1	NBO1_HUMAN
31	151.5	9.3	349	1	LACH_SCHAM
32	150.5	9.2	702	1	CEA5_HUMAN
33	147.5	9.0	1897	1	PTPF_HUMAN

ALIGNMENTS

RESULT 1

ID	JAM2_HUMAN	STANDARD;	PRT;	298 AA.
AC	P57087;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DB	Junctional adhesion molecule 2 precursor (Vascular endothelial			
DB	Junction-associated molecule) (VE-JAM).			
GN	JAM2 OR VEJAM OR C21ORF43.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Vascular endothelial cells;			
RA	MEDLINE=20317114; PubMed=10779521;			
RA	Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;			
RT	"Vascular endothelial junction-associated molecule, a novel member of			
RT	the immunoglobulin superfamily, is localized to intercellular			
RT	boundaries of endothelial cells.";			
RL	J. Biol. Chem. 275:19139-19145(2000).			
EN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	MEDLINE=20507930; PubMed=10945976;			
RA	Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkke R.J.,			
RA	Vanderliffe P., Morris A.P., Brock T.A.;			
RT	"A novel protein with homology to the junctional adhesion molecule:			
RT	Characterization of leukocyte interactions.";			
RL	J. Biol. Chem. 275:34750-34756(2000).			
EN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosch S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

34	146.5	8.9	338	1	LAMP RAT	Q62813	rattus norv
35	145.5	8.9	345	1	OPCM RAT	P32736	rattus norv
36	145.5	8.9	4391	1	PGBM_HUMAN	P98160	homo sapien
37	145	8.9	338	1	LAMP_CHICK	Q98919	gallus gall
38	145	8.9	521	1	CEA1_MOUSE	P31809	mus musculus
39	144.5	8.8	338	1	LAMP_HUMAN	Q13449	homo sapien
40	144	8.8	847	1	CD22_HUMAN	Q20273	homo sapien
41	143.5	8.8	1277	1	CAML_FUGRU	Q98902	fugu rubrip
42	143.5	8.8	1443	1	NEO1_CHICK	Q90610	gallus gall
43	142.5	8.7	646	1	MUI8_HUMAN	P43121	homo sapien
44	142	8.7	365	1	CKAR_MOUSE	P97792	mus musculus
45	141	8.6	345	1	OPCM_BOVIN	P11834	bos taurus

CC -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC SECONDARY LYMPHOID ORGANS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC CELLS.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:1-3(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1652492186.g.htm".
CC
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CC
CC EMBL; AF255910; AAF81223.1; -
CC EMBL; AY016009; AAG49022.1; -
CC EMBL; BC017779; AAH17779.1; -
CC GenBank; HGNC:14686; JAM2.
CC MIM; 606870; -
CC GO; GO:0005887; C:integral to plasma membrane; NAS.
CC GO; GO:0016337; P:cell-cell adhesion; NAS.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 298 JUNCTIONAL ADHESION MOLECULE 2.
FT DOMAIN 21 238 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 239 259 POTENTIAL.
FT DOMAIN 260 298 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 127 IG-LIKE V-TYPE.
FT DOMAIN 134 238 IG-LIKE C2-TYPE.
FT DISULFID 50 109 POTENTIAL.
FT DISULFID 155 214 POTENTIAL.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 298 AA; 33207 MW; CA78E518E22DCAEE CRC64;
Query Match 29.8%; Score 488; DB 1; Length 298;
Best Local Similarity 36.2%; Pred. No. 4.5e-33;
Matches 115; Conservative 60; Mismatches 115; Indels 28; Gaps 10;
QY 1 MALRRPRLCARLPDPFLLILLFRCLIG-----AVNLKSSNRTPVQ--EPSEVELSC 53
DB 1 MARRSRRL-----LLRLYLVALGYKAYGSPAKDQGVVTAVEYQEAALAC 50
QY 54 IITDSQTSPPRIEWKKIQBQTTVFDFNKKIQGLAGRAEILGKTSIKIWNVTRDSALY 113
DB 51 -KTPKKTVSRLSEKKL-GRSVSFVYQQTQLQDFFNRAEMI-DFNIRIKNVTSDAGKY 107
QY 114 RCEVARNDR-KEIDRIVIELTVQVKPVPVPCVRKPAVPVGMKATHLCQSEGHPPHYS 172
DB 108 RCEVAPSQGGQNLIEDTVTLVAVAPVPCSEVPSSALSGTIVELRCQDKGNPAPEVT 167
QY 173 WTRNDVPLTDSRANPRFNSFLNSETGLVFTAVHKDSDQYCIASNDAGSARCE 232
DB 168 WFKDGRILLENPLGSCSNSSYTNATKTGLQFNTVSKLDTGEYSCEARNVGYRCRCP 227
QY 233 QMEVVDNLGTIGIGVVLVAVLALITLIGICAVRRGYFINNKDGESVKNPKPDGVN 292
DB 228 KRMQVDNLNISGIIAAVAVVVALVISGLGVCAQRKGF--SKF--TSFQ----KSNSSS 280
QY 293 YIRTDREGDFRHKSSFI 310

DB 281 KATTSSENDPKRTKSPFI 298
RESULT 2
JAM1_MOUSE
ID JAM1_MOUSE STANDARD; PRT; 300 AA.
AC O88792;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Juncional adhesion molecule 1 precursor (JAM).
GN F1LR OR JAM1 OR JCAM1 OR JCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98327120; PubMed=9660867;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simmons D., Dejana E.;
RT "Junctional adhesion molecule, a novel member of the immunoglobulin
superfamily that distributes at intercellular junctions and modulates
monocyte transmigration.";
RL J. Cell Biol. 142:117-127(1998).
RN [2]
RP INTERACTION WITH PARD3.
RX MEDLINE=21340266; PubMed=11447115;
RA Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
RA Meyer zu Bruckwedde M.-K., Ohno S., Vestweber D.;
RT "The cell polarity protein ASIP/PAR-3 directly associates with
junctional adhesion molecule (JAM).";
RL EMBO J. 20:3738-3748(2001).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX MEDLINE=21391702; PubMed=11500366;
RA Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
RA Winkler F.K., Hennig M.;
RT "X-ray structure of junctional adhesion molecule: structural basis for
homophilic adhesion via a novel dimerization motif.";
RL EMBO J. 20:4391-4398(2001).
CC -!- FUNCTION: Seems to play a role in epithelial tight junction
formation. Appears early in primordial forms of cell junctions and
recruits PARD3. The association of the PARD6-PARD3 complex may
prevent the interaction of PARD3 with JAM1, thereby preventing
tight junction assembly. Plays a role in regulating monocyte
transmigration involved in integrity of epithelial barrier.
CC -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
association between PARD3 and PARD6B probably disrupts this
interaction.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC Localized at tight junctions of both epithelial and endothelial
cells.
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
epithelial and endothelial cells.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U89915; AAC32982.1; -
CC FDB; IF97; 22-AUG-01.
CC MGD; MGI:1321398; F1LR.

DR GO: 0005515; P: protein binding; IPI.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG LIKE; 2.
 DR Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KW Repeat; Signal; 3D-structure.
 FT SIGNAL 1 26
 FT CHAIN 27 300
 FT DOMAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
 FT TRANSMEM 27 238 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 239 259 POTENTIAL.
 FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 28 122 IG-LIKE V-TYPE 1.
 FT DOMAIN 134 230 IG-LIKE V-TYPE 2.
 FT DISULFID 49 108 POTENTIAL.
 FT DISULFID 152 212 POTENTIAL.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32368 MW; 391P3B48FP3B97EC CRC64;
 Query Match 27.9%; Score 457.5; DB 1; Length 300;
 Best Local Similarity 35.6%; Pred. NO. 1.5e-30;
 Matches 106; Conservative 56; Mismatches 121; Indels 15; Gaps 7;
 Qy 20 LLLIFRGLGNAV-----NLSSNFTPVQFESVELSCIITDSQTSPIREWKIQDEQ 74
 Db 11 LLFLFTSMILGSLVQSGSVYTAQSDVQVPEVESIKLTC--TSGFSPRVEMKPVQGST 68
 Qy 75 TTYVFFDNKIQQDLAGRAEILGKTSKTNVTRDSALYRCVARNRDKETDEIVIELT 134
 Db 69 TALVCYNQITAPYADV-TPSSSGITFSSVTRKNGEYTC-WUSEGGQNYGEVSIHLT 126
 Qy 135 VQVPRVTPVCRVPKAVPVGRMATLHCBSGHPHRYMYRNDVPLPT-DSRANPRFRNS 193
 Db 127 VLVPSPKPTISVPSSVTIGNAVLTCSEHDSGPPSEYSEWFGDGLSMLTADAKKTRAFWNS 186
 Qy 194 SFLHNSGTIVTAHVHKGDSQYCIASNDAGSA-RCEQEMEVYDLNIGGIQGLVIV 252
 Db 187 SFTIDPKSGDLIFDPTAFDSGEYTCQAGYGTARSEAAHMDAVELNCGVIAVALVT 246
 Qy 253 LAVLALITLGCACVRRGVFINNKDGSYKXNPKPGDGVNYIRTDGDFRHKSSFVI 310
 Db 247 LILGLLIFGVWPAYSRGVFTTKG-----TAPGKVIYSQPSRSEGEFKTSSFLV 300
 RESULT 3
 ID JAM1 HUMAN
 AC Q9Y624; STANDARD; PRT; 299 AA.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
 DE molecule 1) (PAM-1) (Platelet FII receptor) (UNQ2664/PRO301).
 GN FII1 OR JAM1 OR JCAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99323940; PubMed=10395639;
 RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
 RA Imawatsu A., Kita T.;
 RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
 of junctional adhesion molecule in human endothelial cells.";
 RL J. Immunol. 163:553-557(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genom Res. 13:2265-2270(2003).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=23886257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hsieh L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Seems to play a role in epithelial tight junction
 formation. Appears early in primordial forms of cell junctions and
 recruits PAR3. The association of the PAR3-PAR6 complex may
 prevent the interaction of PAR3 with JAM1, thereby preventing
 tight junction assembly (By similarity). Plays a role in
 regulating monocyte transmigration involved in integrity of
 epithelial barrier. Involved in platelet activation.
 CC -!- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
 association between PAR3 and PAR6B probably disrupts this
 interaction (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
 epithelial and endothelial cells.

RT novel Ig superfamily member from human platelets.";
 RN Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Naik U.P., Naik M.U., DeLeon P., Spychala J.;
 RT "Cloning and characterization of PAM-1, a novel platelet adhesion
 molecule involved in platelet activation.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glaesli S.,
 RA Anselme W., Boecker M., Bloecher H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koshner K., Strack N.,
 RA Mewes H.-W., Ottenwälder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 analysis of 500 novel complete protein coding human cDNAs.";
 RL Genom Res. 11:422-435(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genom Res. 13:2265-2270(2003).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=23886257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hsieh L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Seems to play a role in epithelial tight junction
 formation. Appears early in primordial forms of cell junctions and
 recruits PAR3. The association of the PAR3-PAR6 complex may
 prevent the interaction of PAR3 with JAM1, thereby preventing
 tight junction assembly (By similarity). Plays a role in
 regulating monocyte transmigration involved in integrity of
 epithelial barrier. Involved in platelet activation.
 CC -!- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
 association between PAR3 and PAR6B probably disrupts this
 interaction (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
 epithelial and endothelial cells.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF111713; RAD42050.1; --
 DR EMBL; AF207907; AAF22829.1; --
 DR EMBL; AF172398; RAD48877.1; --
 DR EMBL; AL136649; CAB66584.1; --
 DR EMBL; AY358896; RAO89255.1; --
 DR EMBL; BC001533; RAO01533.1; --
 DR PIR; A59406; S56749.
 DR Genew; HGNC:14685; F1LR.
 DR MIM; 605721; --
 DR GO; GO:0005911; C:intercellular junction; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KW Repeat; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 299 JUNCTIONAL ADHESION MOLECULE 1.
 FT DOMAIN 26 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 259 POTENTIAL.
 FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 27 125 IG-LIKE V-TYPE 1.
 FT DOMAIN 135 228 IG-LIKE V-TYPE 2.
 FT DISULFID 50 109 POTENTIAL.
 FT DISULFID 153 212 POTENTIAL.
 FT CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 25.9%; Score 424; DB 1; Length 299;

Best Local Similarity 32.8%; Pred. No. 8.7e-28; Matches 101; Conservative 48; Mismatches 137; Indels 22; Gaps 7;

QY 8 RLRLCARLPDPFLLLLFRGLICAVNLKSSNRTPVVQEPESVELSCIITDSQTSPIRIFW 67
 DB 9 RKLCLL----FILAILLCSLALGSLVTHSSEVEVRIPENNPVKLSCAY--SGFSSPRVEM 62
 QY 68 KKIODEQTTVPFDDNKIQDLAGRAEILGKTSLKIMNVTTRDSALYRCVAVARNDRKXID 127
 DB 63 KPDQGDITRLVCYNNKITASYEDRVTFLL-PTGITPKSVTREDTGTVC-MVSEEGGNSYG 120
 QY 128 EIVILTVQKVTVCVRPKAVPGKMATLHQSSEGHPRPHYSYRNDVPLPTDSRAN 187
 DB 121 EYVKVLLVLPSPKPTVNPSSATTGNRAVLTCSEBODGPPSEYTFMFKDGIYVNPCKST 180
 QY 188 PFRNSSPHLNSGTGLVTAHVKKDSDGOYCIASNDAGSARCEQ-EMEVDLMTIGGII 246
 DB 181 RAPSNSVYLVNPTTGELVFDPLISADTGEYSCEARNGYGTPTMSNAVRMEAVERNVGIV 240
 QY 247 GGVLVVLAVALITIGICAYRGGVFINNKQGES-----YRNGKPDGVNYIRTBEGDF 302
 DB 241 AAVLVTLILGILVFGIPAYSRGHFDRTKGTSSRKVTYSQPS-----ARSEGEF 291
 QY 303 RHKSSPVI 310
 DB 292 KOTSSFLV 299

RESULT 4

JAM1_BOVIN

ID JAM1_BOVIN STANDARD; PRT; 298 AA.

AC Q9XT56;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE JUNCTIONAL adhesion molecule 1 precursor (JAM).
 GN F1LR OR JAM1.
 OS Bos taurus (Bovine).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Rutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99323940; PubMed=10395639;
 RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
 RA Iwamatsu A., Kita T.;
 RT Combined treatment of TNF-alpha and IFN-gamma causes redistribution
 RT of junctional adhesion molecule in human endothelial cells.;
 RL J. Immunol. 163:553-557(1999).
 CC -!- FUNCTION: Seems to plays a role in epithelial tight junction
 CC formation. Appears early in primordial forms of cell junctions and
 CC recruits PAR3. The association of the PAR3-PAR3 complex may
 CC prevent the interaction of PAR3 with JAM1, thereby preventing
 CC tight junction assembly (By similarity). Plays a role in
 CC regulating monocyte transmigration involved in integrity of
 CC epithelial barrier. Involved in platelet activation.
 CC -!- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
 CC association between PAR3 and PAR3B probably disrupts this
 CC interaction (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
 CC epithelial and endothelial cells.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -----
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 CC -----
 CC EMBL; AF111714; RAD42051.1; --
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003598; IG_c2.
 CC Pfam; PF00047; Ig; 2.
 CC SMART; SM00408; Igc2; 1.
 CC PROSITE; PS50835; IG LIKE; 2.
 KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KW Repeat; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 298 JUNCTIONAL ADHESION MOLECULE 1.
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 298 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 28 134 IG-LIKE V-TYPE 1.
 FT DOMAIN 134 227 IG-LIKE V-TYPE 2.
 FT DISULFID 49 108 POTENTIAL.
 FT DISULFID 152 211 POTENTIAL.
 FT CARBOHYD 184 184 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 298 AA; 32456 MW; 71AFBIC1714769A2 CRC64;
 Query Match 25.0%; Score 408.5; DB 1; Length 298;
 Best Local Similarity 33.8%; Pred. No. 1.6e-26;
 Matches 102; Conservative 49; Mismatches 124; Indels 27; Gaps 10;
 QY 21 LLLFRGLI-----GAVNLKSSNRTPVVQ--EPESVELSCIITDSQTSPIRIFW 71
 DB 12 LLLFTSMILCSLALGRGAV-----QTYEPVVRVPPNNPAKLSC--SYSGFSSPRVWKPTH 65
 QY 72 DEQTTVPFDDNKIQDLAGRAEILGKTSLKIMNVTTRDSALYRCVAVARNDRKXID 131

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Db 66 GDRLGVCNNKKTASYENRV-TFSDTGITFHSVTRKDTGMYTC-MVSDGGNTVGEVTV 123
Qy 132 ELTVQVKVTPVCRVPEKAVPVGKMATLHCQSEGEHPRPHYSWYRNDVPLPDTDSRANPRFR 191
Db 124 QLIVLVPSPKPTINVPSSVTITGTRAVLTCSESDGSPPEYKFKDGVEMPLEPKSNRAP 183
Qy 192 NSSPHLNSSETGLVFTAVHKDQSGQYCIASND-AGSARCEQEMEVVDNLNIGGIIIGVL 250
Db 184 NSSYTLNQKTGELIIFDPVSASDTGFTCOAQNGYASPVKSDTVHMDAVELNNGGIVAAVP 243
Qy 251 VVLVALILITGICCAVRYGPIPNKODGESYKPKGPDGVNVIIRD--EEGDFRHKSP 308
Db 244 VTLILGALIGFIWFAYSRGIFDRAK-GTSNKK-----VIYSPNARSDEFRQTSSP 296
Qy 309 VI 310
Db 297 LV 298

RESULT 5
ID - A33 HUMAN STANDARD; PRT; 319 AA.
AC Q95795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Colon carcinoma;
RA MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474 (1997).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium."
RL Biochem. Biophys. Res. Commun. 236:682-686 (1997).
CC -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC CARBOHYDRATE.
CC -!- PTM: Palmitoylated.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC -----
DR EMBL; U79725; AAC50957.1; -.
DR Genew; HGNC:4445; GPA33.

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DR MIM: 602171; -.
DR GO: GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO: GO:0004872; F:receptor activity; TAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_2.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319 CELL SURFACE A33 ANTIGEN.
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 319 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 134 IG-LIKE V-TYPE.
FT DOMAIN 140 227 IG-LIKE C2-TYPE.
FT DOMAIN 258 261 POLY-CYS.
FT DISULFID 43 117 POTENTIAL.
FT DISULFID 146 222 POTENTIAL.
FT DISULFID 162 211 N-LINKED (GLCNAC. . .).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408B CRC64;

Query Match 14.0%; Score 228.5; DB 1; Length 319;
Best Local Similarity 25.7%; Pred. No. 1.3e-11;
Matches 79; Conservative 49; Mismatches 128; Indels 51; Gaps 14;

Qy 29 IGAVNLKSNRTPVVOBPESVELSCII-TDSQTSPPRIEWKKIQDSQTVVP---PDNK- 83
Db 19 VDAISVETPDQVLRASQGSQSVLPTCTYHTSTSRGLIQMDKLLLTHTRVVIWPFSEN 78
Qy 84 -IQGDL-----AGRAELTGKTSKIMVNRDSDALYRCEVVARNDKEIDIVELTV 135
Db 79 YHGEIYKRVISINNAE-QSDASITDQLTWADNGTYESVLSMDLEGTKSRVLLV 137
Qy 136 QVKVTPVCRVPEKAVPVGKMATLHCQSEGEHPRPHYSWYRNDV-----PLPTDSRANPRF 190
Db 138 LVPPSKPEGIGETIIGNNIQLTQSKSGSPTPQYSWKRYNLNQEQLAQPASGQP-- 195
Qy 191 RNSSPHLNSSETGLVFTAVHKDQSGQYCIASNDAGSARCE-EQEMEVVDNLNIG---GII 246
Db 196 -----VSLKNISTDTSYICTSSNEGTFQCNITVAVRSFMSMVALYVGLA 242
Qy 247 GGVVLVLAVALITLIGICCAVRYGPIN--NKQDG-----ESYKNPKGPDGVNVI--RTDE 298
Db 243 VGVVAALLIIGIIYCCCC---RGKDDNTDEKEDARPNEAYEEP--PQLRELSRERE 297
Qy 299 EGDPRHK 305
Db 298 EDDYRQE 304

RESULT 6
ID NCAL XENLA STANDARD; PRT; 1088 AA.
AC P16170;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
DE 180).
DE NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180).
RX MEDLINE=90098871; PubMed=2481269;

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DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; 1g; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS00835; IG_LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1092
FT
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1092
FT DOMAIN 20 108
FT DOMAIN 113 202
FT DOMAIN 208 295
FT DOMAIN 303 397
FT DOMAIN 400 489
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 373
FT DISULFID 420 479
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
SQ SEQUENCE 1092 AA; 118082 MW; CD236E0E9F987AD1 CRC64;

Query Match 10.8%; Score 177; DB 1; Length 1092;
Best Local Similarity 28.6%; Pred. No. 1e-06;
Matches 60; Conservative 28; Mismatches 88; Indels 34; Gaps 10;

QY 30 GAVNLKSSNR-----TPVQVPESEVELSCIIITSDTSQPR-LEWK-KIQDQQTIVVFQDN 82
DB 105 GTVNLKIQKLTQKFKYAPTQPETEGEDAVICDVSSIPSIITWRHKGK-----VIFPK 159
QY 83 KIQGLAGRAEILGKSLKINWVRDSDALVRC--VVARNDKKEIDELVIELTVQVQKPV 140
DB 160 DV-----RFVVLANNYLQIRGKIKKIDEGNYRCEGRILARG---EINYKDIQIVTVNPPL 210
QY 141 TPV--CRVPKAVPGVGMAATLHCOESEGHPHRYSWYRNDVPLPTDSRANPRFNSFFHLN 198
DB 211 IQARQIRVNATANDSESVVLSG-DADGPDPEISWIKKEPTEDG-----EEKISFN 261
QY 199 SETGTLVFTAVHKDSGGQYICIASNDAGSA 228
DB 262 EDKSEMTIYRVEKDEAEYSYCIANNQAGEA 291

RESULT 8
AMAL DROME
ID AMAL DROME STANDARD; PRT; 333 AA.
AC P15364; Q9V3A5;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amalgam protein precursor.
GN AMA OR BG:DS00276.6 OR CG2198.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Oregon-R;
RX MEDLINE=89028670; PubMed=3141062;
RA Seeger M.A., Haffley L., Kaufman T.C.;
RT "Characterization of amalgam: a member of the immunoglobulin
RL superfamily from Drosophila.";
RL Cell 55:589-600(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Celniker S.B., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
RA Palazzolo M.J.;
RL "Complete sequence of the Antennapedia complex of Drosophila.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis J.M., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner B.C., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Embryo;
MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.B.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH080.1-RESEARCH080.8(2002).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC -----
 DR EMBL; M23561; AAA28367.1; --
 DR EMBL; AE001572; AAD19797.1; --
 DR EMBL; AE003674; AAP54084.1; --
 DR EMBL; AY051911; AAK93335.1; --
 DR PIR; A31923; A31923.
 DR FlyBase; FBgn0000071; Ama.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 KW Immunoglobulin domain; Glycoprotein; Membrane; GPI-anchor; Signal;
 KW Repeat.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 ? AMALGAM PROTEIN.
 FT PROPEP ? 333 REMOVED IN MATURE FORM (POTENTIAL).
 FT DOMAIN 25 128 IG-LIKE V-TYPE.
 FT DOMAIN 139 223 IG-LIKE C2-TYPE 1.
 FT DOMAIN 230 323 IG-LIKE C2-TYPE 2.
 FT DISULFID 46 117 PROBABLE.
 FT DISULFID 161 208 PROBABLE.
 FT DISULFID 251 307 PROBABLE.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 83 83 Q -> K (IN REF. 1).
 SQ SEQUENCE 333 AA; 36387 MW; F644753DE3DB25F1 CRC64;

Query Match 10.6%; Score 174; DB 1; Length 333;

Best Local Similarity 26.3%; Pred. No. 4.2e-07;

Matches 51; Conservative 39; Mismatches 84; Indels 20; Gaps 5;

QY 35 KSNRTVPVQEFSEVSLSCITSDSPRIEMKKIQDEQTYVFFDNKIQDLAGRAHI 94
 Db 143 ENTPKSTLVTEGQNLCTC--HANGFPKPTISWAR-----EHNAMVPAGGHL 187
 QY 95 LGKTSLKUNVTRDSALYRCEVARNDRKDEIVIELTVQVPTVCVRPKAVPVGK 154
 Db 188 LAEPTLIRSVHRMDGGYYC--IAQNGEGQPKLIRVEFRPQIAVQRPKIAQMVSH 245
 QY 155 MATLHQEGEGHPRPHYSVYRNDVPLPTDSRAMPFRNRSFHLNSETGLVFTAVHKDSS 214
 Db 246 SAELEC-SVQGYPAPTVWHKGVPL--QSSRHEVANTASSSGTTTSVLRIIDSUGEDP 302
 QY 215 GQYICIASNDAGSA 228
 Db 303 GDYYCNATNKLGH 316

RESULT 9

NCB2 MOUSE
 ID NCA2 MOUSE STANDARD; PRT; 725 AA.
 AC P13594; Q61950;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neutral cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
 DE (NCAM-120).
 GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=87246524; PubMed=3595563;
 RA Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,

RA Hirsch M.-R., Pontecilla-Camps J.-C., Goridis C.;
 RT "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
 RT a Mr 79,000 polypeptide without a membrane-spanning region.";
 RL EMBO J. 6:907-914(1987).
 RN [2]
 RP SEQUENCE OF 20-700 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=89251563; PubMed=2721486;
 RA Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
 RT "Differential exon usage involving an unusual splicing mechanism
 RT generates at least eight types of NCAM cDNA in mouse brain.";
 RL EMBO J. 8:385-392(1989).
 RN [3]
 RP SEQUENCE OF 642-725 FROM N.A.
 RC MEDLINE=88283628; PubMed=3396534;
 RA Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
 RT "Differential splicing and alternative polyadenylation generates
 RT distinct NCAM transcripts and proteins in the mouse.";
 RL EMBO J. 7:625-632(1988).
 RN [4]
 RP SEQUENCE OF 20-36.
 RC MEDLINE=86140120; PubMed=3512556;
 RX Rougon G., Marshak D.R.;
 RA "Structural and immunological characterization of the amino-terminal
 RT domain of mammalian neural cell adhesion molecules.";
 RL J. Biol. Chem. 261:3396-3401(1986).
 CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
 CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
 CC neurites, etc.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=N-CAM 120;
 CC IsoId=P13594-1; Sequence=Displayed;
 CC Name=N-CAM 180;
 CC IsoId=P13595-1; Sequence=External;
 CC Name=N-CAM 140;
 CC IsoId=P13598-2; Sequence=External;
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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EMBL; Y00051; CAA68263.1; --
 EMBL; X15049; CAA33148.1; AUT_SEQ.
 EMBL; X07195; CAA30173.1; --
 PIR; A29673; IJMSNG.
 PDB; 3NCM; 12-MAR-97.
 PDB; 3NCM; 23-JUL-99.
 MGD; MGI:97281; Ncaml.
 InterPro; IPR008957; FN_III-like.
 InterPro; IPR003961; FN_III.
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003598; Ig_c2.
 Pfam; PF00041; fn3; 2.
 Pfam; PF00047; Ig; 5.
 SMART; SM00060; FN3; 2.
 SMART; SM00408; IGC2; 5.
 PROSITE; PS50835; IG LIKE; 5.
 Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
 Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
 3D-structure. 1 19
 SIGNAL
 CHAIN 20 725
 DOMAIN 20 111
 DOMAIN 116 205
 NEURAL CELL ADHESION MOLECULE 1, 120 kDa
 ISOFORM.
 IG-LIKE C2-TYPE 1.
 IG-LIKE C2-TYPE 2.

Best Local Similarity 31.5%; Pred. NO. 4.2e-06;
Matches 62; Conservative 20; Mismatches 69; Indels 46; Gaps 9;

Qy 47 BVELSCIIITDSQSDPIEWKIKDEQTVVFDNKLQGLAGRAEILGKTSLKINWVT 106
Db 233 QSAVLPCVA--SGLPAPVIRWKKEDVLDT-----SSGRLALLAGSLEISDVT 280
Qy 107 RDSALYRCVVARNDKREIDIEIVIELTVQVKVPTVPCVRKAVPVGKQATLHCOES--- 163
Db 281 EDDAGTYFC--VADNGKTI-BAQAEITVQVPPPEF-----LKQPAIYARESMDI 327
Qy 164 -----EGHPHYSWYRN-DVPLPTDSRANPRFNSPHLNSSETGTLVFTAVHKDQSGQ 216
Db 328 VFECEVTGKPAFTVKNVKGWIPSD-----YFKIVKEHNLQVLGLV-KSDRGF 376
Qy 217 YYCIIASNDAGSARCEBQ 233
Db 377 YQCIANDVGNQAQAQ 393

RESULT 12
NCM2 HUMAN STANDARD; PRT; 837 AA.
AC O15394;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2).
GN NCM2 OR NCM21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369930; PubMed=9226371;
RA Paoloni-Giacobino A., Chen H., Antonarakis S.B.;
RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)
that maps to chromosome region 21q21 and is potentially involved in
Down syndrome.";
RL Genomics 43:43-51(1997).
RN [2]
RP CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebbersold R.;
RT "Identification and quantification of N-linked glycoproteins using
hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: May play important roles in selective fasciculation and
zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
brain.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U75330; AAB80803.1; --
DR Genbank; HGNC:7657; NCM2.
DR MIM; 602040; --
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0007158; P:neuronal cell adhesion; TAS.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 837
FT DOMAIN 20 697
FT TRANSMEM 598 718
FT DOMAIN 719 837
FT DOMAIN 21 108
FT DOMAIN 113 202
FT DOMAIN 208 297
FT DOMAIN 302 396
FT DOMAIN 401 491
FT DOMAIN 482 581
FT DOMAIN 594 678
FT DISULFID 42 93
FT DISULFID 136 186
FT DISULFID 232 281
FT DISULFID 322 380
FT DISULFID 422 475
FT CARBOHYD 219 177
FT CARBOHYD 219 309
FT CARBOHYD 309 319
FT CARBOHYD 406 406
FT CARBOHYD 419 419
FT CARBOHYD 445 445
FT CARBOHYD 474 474
FT CARBOHYD 562 562
SQ SEQUENCE 837 AA; 92932 MW; C3D034106C5741C1 CRC64;

Query Match 10.4%; Score 170; DB 1; Length 837;
Best Local Similarity 24.3%; Pred. No. 2.8e-06;
Matches 72; Conservative 32; Mismatches 104; Indels 88; Gaps 15;

Qy 44 QEP---BVELSCIIITDSQSDPIEWKIKDEQTVVFDNKLQGLAGRAEILGKTSL 100
Db 124 QEPKQGEDAEVVCVSSSPA--PAVSMLYHNEEVT--ISDN-----RLAHLANNML 171
Qy 101 KIWNVTRDSALYRC--VVARNDKREIDIEIVIELTVQVKVPTVPCVRKAVPV----- 152
Db 172 QILNINKSDEGIYRCGRVARGE-----IDPRDIIVIVNVPVPAISMFOKSFN 219
Qy 153 -----GKWTALHCOESGHPHYSWYRNDVPLPTDSRANPRFNSPHLNSSETGTLVFT 207
Db 220 ATAERGEEMTFSRAS--GSPEPAISWPRNGKLI-----ENEKYLKGSNTELTVR 269
Qy 208 AVHKDDSQYCIASNDAGSARCEBQEMVVDNLNIGGIIGVVLVLAVALITLIGCCAY 267
Db 270 NIINSDGGPYVCRAINKAG-----EDEKQAP-----LQVFPVPHIQLKNETTY 313
Qy 268 RRGVFINNKQGESYTNPKP-----DGWVYRTDDEGDFR-----HKSS 307
Db 314 ENQGVTLVCDAE-----GSPITEITWRAVDGPTFTTEGDKSPDGRIEVKGHGSS 363

RESULT 13
NCAL RAT STANDARD; PRT; 858 AA.
AC P13596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140).
DE (NCAM-140).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=88059265; PubMed=3680385;
 RA Small S.J., Shull G.B., Santoni M.-J., Akesson R.;
 RT "Identification of a cDNA clone that contains the complete coding
 RT sequence for a 140-kD rat NCAM polypeptide.";
 RL J. Cell Biol. 105:2335-2345(1987).
 RN [2]
 RP SEQUENCE OF 355-364 FROM N.A.
 EX MEDLINE=90166485; PubMed=2483093;
 RA Small S.J., Haines S.L., Akesson R.A.;
 RT "Polypeptide variation in an N-CAM extracellular immunoglobulin-like
 RT fold is developmentally regulated through alternative splicing.";
 RL Neuron 1:1007-1017(1988).
 CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
 CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
 CC neurites, etc.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;
 CC IsoId=P13396-1; Sequences=Displayed;
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL; X06564; CAA29809.1; -;
 DR EMBL; M32611; AAA41679.1; -;
 DR PIR; S00846; IJRTNC.
 DR PDB; 1BPP; 27-OCT-00.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN-III.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; ig; 5.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00408; IGC2; 5.
 DR PROSITE; PS50835; IG_LIKE; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
 KW 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 858
 FT NEURAL CELL ADHESION MOLECULE 1, 140 kDa
 FT ISOFORM.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 722 739
 FT DOMAIN 740 858
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 20 111
 FT IG-LIKE C2-TYPE 1.
 FT DOMAIN 116 205
 FT IG-LIKE C2-TYPE 2.
 FT DOMAIN 212 302
 FT IG-LIKE C2-TYPE 3.
 FT DOMAIN 309 414
 FT IG-LIKE C2-TYPE 4.
 FT DOMAIN 417 502
 FT IG-LIKE C2-TYPE 5.
 FT DOMAIN 514 615
 FT FIBRONECTIN TYPE-III 1.
 FT DOMAIN 616 712
 FT FIBRONECTIN TYPE-III 2.
 FT DOMAIN 152 156
 FT HEPARIN-BINDING (POTENTIAL).
 FT DOMAIN 161 165
 FT HEPARIN-BINDING (POTENTIAL).
 FT DISULFID 41 96
 FT BY SIMILARITY.
 FT DISULFID 139 189
 FT BY SIMILARITY.
 FT DISULFID 235 288
 FT BY SIMILARITY.
 FT DISULFID 330 396
 FT BY SIMILARITY.
 FT DISULFID 437 490
 FT BY SIMILARITY.

FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 858 AA; 94658 MW; EALA06A4EA0550F6 CRC64;
 Query Match 10.4%; Score 169.5; DB 1; Length 858;
 Best Local Similarity 26.3%; Pred. No. 3.2e-06;
 Matches 61; Conservative 42; Mismatches 84; Indels 45; Gaps 12;
 QY 27 CLIGA-----VNLKSSNR-----TPVQEPESVELSCIITDSQTS-DPIREKKIQ 71
 DB 96 CVTRADGTQSEATNVKIFKLMFNKAPFQEFKEGDAIVCVWSLPTLWK--- 152
 QY 72 DEQTTYVPFDNKIQGLAGRAIILGKTSLKINVTFRDSALYRCE--VVARNDKKEIDSI 129
 DB 153 -----HKGRDVLKKDV--RPVLSNNYLQIRGIKKTDEGTYRCGRILARG---EINFK 202
 QY 130 VIETVQYKVPVPCVCR--VPKAVPVGMATLHCQSEGHPRPHYSWYRNDVPLPTDSRAN 187
 DB 203 DIQIVNVPPPTVQARQISVNTANILGQSVTLVC-DADGFPETMGTDKDGFPIENEEDD 261
 QY 188 PRFRNSSPHL-NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCCEQKEVY 238
 DB 262 EK-----HIFSDSSSELTIRNVNDKNDKAEYVCIAENRAG-----EQDASIH 302
 RESULT 14
 ID PTPD HUMAN STANDARD; PRT; 1912 AA.
 DT P23468;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
 DE delta).
 DE PTPRD.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
 RX MEDLINE=95204468; PubMed=7896816;
 RA Fulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
 RT "Molecular characterization of the human transmembrane protein-
 RT tyrosine phosphatase delta. Evidence for tissue-specific expression of
 RT alternative human transmembrane protein-tyrosine phosphatase delta
 RT isoforms.";
 RL J. Biol. Chem. 270:6722-6728(1995).
 RN [2]
 RP SEQUENCE OF 390-1912 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=91006018; PubMed=2170109;
 RT Krueger N.X., Streuli M., Saito H.;
 RT "Structural diversity and evolution of human receptor-like protein
 RT tyrosine phosphatases.";
 RL EMBO J. 9:3241-3252(1990).
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P23468-1; Sequences=Displayed;
 CC Name=2; Synonyms=Kidney;
 CC IsoId=P23468-2; Sequences=VSP_005147, VSP_005148, VSP_005149;
 CC Name=3; Synonyms=Petal brain;
 CC IsoId=P23468-3; Sequences=VSP_005150;
 CC -!- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 15, 2004, 10:58:19 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-15

Perfect score: 1637

Sequence: 1 MALRRPRLRLCARLPDFL.....VNYRTDEGDFRUKSFSVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1637	100.0	310	4 Q9BX67	Q9bx67 homo sapien
2	1637	100.0	355	4 Q8WXL8	Q8wxl8 homo sapien
3	1628	99.5	309	4 Q96PL1	Q96pl1 homo sapien
4	1425	87.0	310	11 Q9D8B7	Q9d8b7 mus musculus
5	1423	86.9	310	11 Q9EPK4	Q9epk4 mus musculus
6	1411	86.2	310	11 Q9D1M9	Q9d1m9 mus musculus
7	486.5	29.7	298	11 Q9J159	Q9j159 mus musculus
8	486.5	29.7	298	11 Q9C5K9	Q9c5k9 mus musculus
9	483.5	28.5	298	11 Q9CE95	Q9ce95 mus musculus
10	463.5	28.3	300	11 Q9JHY1	Q9jhy1 rattus norv
11	460	28.1	289	13 Q7ZW70	Q7zw70 xenopus lae
12	457.5	27.9	300	11 Q9VC39	Q9vc39 mus musculus
13	440.5	26.9	300	13 Q7SYQ7	Q7syq7 xenopus lae
14	336	20.5	259	4 Q9Y5B2	Q9y5b2 homo sapien
15	326	19.9	173	11 Q9JKD5	Q9jkd5 rattus norv
16	291	17.8	64	11 Q8BT59	Q8bt59 mus musculus

17	243.5	14.9	304	11 Q9CVA4	Q9cva4 mus musculus
18	242	14.8	318	13 Q91664	Q91664 xenopus lae
19	242	14.8	327	4 Q96IQ7	Q96iq7 homo sapien
20	240.5	14.7	284	4 Q9NX42	Q9nx42 homo sapien
21	240.5	14.7	325	4 Q95791	Q95791 homo sapien
22	233.5	14.3	328	11 Q92109	Q92109 mus musculus
23	221.5	13.5	319	11 Q922D5	Q922d5 mus musculus
24	216	13.2	407	11 Q9D2J4	Q9d2j4 mus musculus
25	215.5	13.2	319	11 Q9JKA5	Q9jka5 mus musculus
26	206.5	12.6	248	11 Q9D0T4	Q9d0t4 mus musculus
27	206.5	12.6	335	13 Q9PWR4	Q9pwr4 gallus gall
28	203.5	12.4	335	13 Q9YGH1	Q9ygh1 gallus gall
29	203	12.4	181	13 Q91655	Q91655 xenopus lae
30	199.5	12.2	372	13 Q90Y50	Q90y50 brachydanio
31	198.5	12.1	335	13 Q9YGV5	Q9ygv5 gallus gall
32	197.5	12.1	387	4 Q9H6B4	Q9h6b4 homo sapien
33	193.5	11.8	373	4 Q9H6B4	Q9h6b4 homo sapien
34	193.5	11.8	795	13 Q90YM0	Q90ym0 brachydanio
35	189.5	11.6	358	13 Q90490	Q90490 brachydanio
36	188.5	11.5	1409	13 Q8J127	Q8j127 brachydanio
37	188.5	11.5	1409	13 Q801M2	Q801m2 brachydanio
38	188.5	11.5	1428	13 Q8AY67	Q8ay67 brachydanio
39	188	11.5	259	4 Q7Z2Q1	Q7z2q1 homo sapien
40	187.5	11.5	838	13 Q90YML	Q90yml brachydanio
41	187	11.4	725	13 Q73633	Q73633 xenopus lae
42	182.5	11.1	372	11 Q8K1G0	Q8k1g0 rattus norv
43	180.5	11.0	300	11 Q9DA22	Q9da22 mus musculus
44	180.5	11.0	300	11 Q9D9J0	Q9d9j0 mus musculus
45	180.5	11.0	1894	11 Q64487	Q64487 mus musculus

ALIGNMENTS

RESULT 1

Q9BX67	PRELIMINARY;	PRT;	310 AA.
ID Q9BX67	PRELIMINARY;	PRT;	310 AA.
AC Q9BX67	01-JUN-2001 (TREMBLrel. 17, Created)		
DT 01-JUN-2001	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT 01-OCT-2003	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein FLJ90288) (Hypothetical protein FLJ90828).			
DE FLJ90288	JAM-2 OR JAM3.		
GN JAM-2 OR JAM3.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
[1] SEQUENCE FROM N.A.			
RP TISSUE=Brain;			
RC Cunningham S.A., Arrate M.P., Tran T.M.;			
RT "Cloning of Human Junctional Adhesion Molecule 3.";			
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
[2] SEQUENCE FROM N.A.			
RP Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;			
RT "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members.";			
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
[3] SEQUENCE FROM N.A.			
RP Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;			
RT "Junctional adhesion molecules (JAMs) and interendothelial junctions.";			
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
[4] SEQUENCE FROM N.A.			
RP Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;			
RT "Characterization of Junctional Adhesion Molecule-3 on Human Platelets: A New Member of Immunoglobulin Superfamily.";			

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RN [5]
 RP SEQUENCE FROM N.A.
 RA Isegai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saïto K.,
 RA Yamamoto J., Makamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
 RA "NEO human cDNA sequencing project."
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF356518; AK27221.1; -
 DR EMBL; AJ344431; CAC69845.1; -
 DR EMBL; AF448478; AAM20925.1; -
 DR EMBL; AK074769; BAC11195.1; -
 DR EMBL; AK075309; BAC11538.1; -
 DR InterPro: IPR007110; Ig-like.
 DR Pfam: PF00047; ig; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 30
 SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EALDAB9 CRC64;

Query Match 100.0%; Score 1637; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 3.8e-153;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
 DB 1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
 QY 61 SDPRIEWKKIQDEQTYVFDNKKIQDLAGRAELIGKTSLKINVTTRDSALYRCVVAR 120
 DB 61 SDPRIEWKKIQDEQTYVFDNKKIQDLAGRAELIGKTSLKINVTTRDSALYRCVVAR 120
 QY 121 NRKKEIDEIVIELTVQVKPTVCRVPKAVPVGKMATLHCQSESGHPRPHYSYRNDVPL 180
 DB 121 NRKKEIDEIVIELTVQVKPTVCRVPKAVPVGKMATLHCQSESGHPRPHYSYRNDVPL 180
 QY 181 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDGGQYCIASNDAGSARCEQEEMEYVDL 240
 DB 181 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDGGQYCIASNDAGSARCEQEEMEYVDL 240
 QY 241 NGGIIGGVVLVLAVALITLIGCCAYRRGYFINNKDGESYKPKGPGGVNVRTDEEG 300
 DB 241 NGGIIGGVVLVLAVALITLIGCCAYRRGYFINNKDGESYKPKGPGGVNVRTDEEG 300
 QY 301 DFRHKSSPVI 310
 DB 301 DFRHKSSPVI 310

RESULT 2

Q8WVL8 PRELIMINARY; PRT; 355 AA.
 AC Q8WVL8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Junction adhesion molecule 3.
 GN JAM3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hearn T.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Phillips H.M.;
 RT "Narrowing the critical region within 11q24-qter for hypoplastic left heart and identification of a candidate gene, JAM3, expressed during

RT cardiogenesis.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ416101; CAC94776.1; -
 DR Genew; HGNC:15532; JAM3.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 FT CHAIN 76 355
 SQ SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

Query Match 100.0%; Score 1637; DB 4; Length 355;
 Best Local Similarity 100.0%; Pred. No. 4.6e-153;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
 DB 46 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 105
 QY 61 SDPRIEWKKIQDEQTYVFDNKKIQDLAGRAELIGKTSLKINVTTRDSALYRCVVAR 120
 DB 106 SDPRIEWKKIQDEQTYVFDNKKIQDLAGRAELIGKTSLKINVTTRDSALYRCVVAR 165
 QY 121 NRKKEIDEIVIELTVQVKPTVCRVPKAVPVGKMATLHCQSESGHPRPHYSYRNDVPL 180
 DB 166 NRKKEIDEIVIELTVQVKPTVCRVPKAVPVGKMATLHCQSESGHPRPHYSYRNDVPL 225
 QY 181 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDGGQYCIASNDAGSARCEQEEMEYVDL 240
 DB 226 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDGGQYCIASNDAGSARCEQEEMEYVDL 285
 QY 241 NGGIIGGVVLVLAVALITLIGCCAYRRGYFINNKDGESYKPKGPGGVNVRTDEEG 300
 DB 286 NGGIIGGVVLVLAVALITLIGCCAYRRGYFINNKDGESYKPKGPGGVNVRTDEEG 345
 QY 301 DFRHKSSPVI 310
 DB 346 DFRHKSSPVI 355

RESULT 3

Q96FLI PRELIMINARY; PRT; 309 AA.
 AC Q96FLI;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUES=Eye;
 RC Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010690; AAH10690.1; -
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Hypothetical protein; Immunoglobulin domain.
 FT NON_TER 1
 SQ SEQUENCE 309 AA; 34917 MW; 50C5B1B787E8DF3 CRC64;

Query Match 99.5%; Score 1628; DB 4; Length 309;
 Best Local Similarity 99.7%; Pred. No. 3e-152;
 Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


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Qy 2 ALRRPPRLRLCARLPDPFLILLFRGLIGAVNLKSSNRTTPVQBPESVELSCIITDSQTS 61
Db 1 ALRRPPRLRLCARLPDPFLILLFRGLIGAVNLKSSNRTTPVQBPESVELSCIITDSQTS 60
Qy 62 DPRIEWKKIQBQOTTYVFDNKKIQDLAGRAEILGKTSKIMVTRRDSALYRCVWVARN 121
Db 61 DPRIEWKKIQBQOTTYVFDNKKIQDLAGRAEILGKTSKIMVTRRDSALYRCVWVARN 120
Qy 122 DRKEIDEIVIELTVQVKPVPVCRPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPLP 181
Db 121 DRKEIDEIVIELTVRVPKVPVCRPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPLP 180
Qy 182 TDSRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYCIASNDAGSARCEQMEVYDLN 241
Db 181 TDSRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYCIASNDAGSARCEQMEVYDLN 240
Qy 242 IGGIIGGVVLVAVLALITLIGCCAYRGYFNNKQDGESYKNGPKDGVNVIETDERGD 301
Db 241 IGGIIGGVVLVAVLALITLIGCCAYRGYFNNKQDGESYKNGPKDGVNVIETDERGD 300
Qy 302 FRHKSSPVI 310
Db 301 FRHKSSPVI 309

RESULT 4
Q9DBB7 PRELIMINARY; PRT; 310 AA.
ID AC Q9DBB7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional cell adhesion molecule-2, JAM-2 (1110002N23Rik protein)
GN JCAM3 OR JCAM2 OR JCAM2 OR 1110002N23RIK
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR ENBL; AK008187; BAB25519.1;
DR InterPro; IPR007110; IG-like.
DR DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

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Query Match 87.0%; Score 1425; DB 11; Length 310;
 Best Local Similarity 86.5%; Pred. No. 3.4e-132;

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Matches 268; Conservative 19; Mismatches 23; Indels 0; Gaps 0;
Qy 1 MALRRPPRLRLCARLPDPFLILLFRGLIGAVNLKSSNRTTPVQBPESVELSCIITDSQTS 60
Db 1 MALRRPPRLRLCARLPDPFLILLFRGLIGAVNLKSSNRTTPVQBPESVELSCIITDSQTS 60
Qy 61 SDPRIEWKKIQBQOTTYVFDNKKIQDLAGRAEILGKTSKIMVTRRDSALYRCVWVARN 120
Db 61 SDPRIEWKKIQBQOTTYVFDNKKIQDLAGRAEILGKTSKIMVTRRDSALYRCVWVARN 120
Qy 121 NDRKEIDEIVIELTVQVKPVPVCRPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQVKPVPVCRPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPL 180
Qy 181 PTDGRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYCIASNDAGSARCEQMEVYDL 240
Db 181 PTDGRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYCIASNDAGSARCEQMEVYDL 240
Qy 241 MIGGIIGGVVLVAVLALITLIGCCAYRGYFNNKQDGESYKNGPKDGVNVIETDERG 300
Db 241 MIGGIIGGVVLVAVLALITLIGCCAYRGYFNNKQDGESYKNGPKDGVNVIETDERG 300
Qy 301 DFRHKSSPVI 310
Db 301 DFRHKSSPVI 310

RESULT 5
Q9EPK4 PRELIMINARY; PRT; 310 AA.
ID AC Q9EPK4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional cell adhesion molecule-2, JAM-2 (1110002N23Rik protein)
GN JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

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RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
 RA Trusberg R.;
 RN Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
 RX MEDLINE=2234683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT. "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AJ300304; CAC20704.1; -;
 DR EMBL; AK013156; BAB28683.1; -;
 DR EMBL; BC024357; AAH24357.1; -;
 DR EMBL; AK032833; BAC28049.1; -;
 DR MGD; MGI:1933825; Jam3.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig_2.
 DR SMART; SM00408; Igc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;

Query Match 86.9%; Score 1423; DB 11; Length 310;
 Best Local Similarity 86.5%; Pred. No. 5.4e-132;
 Matches 268; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY 1 MALRPPRLRLCARLPDPFLLLFRGCLIGAVNLKSSNRPVQPFESVELSCIITDSQT 60
 DB 1 MALSRRLRLRLYARLPDPFLLLFRGCLIGAVNLKSSNRPVQPFESVELSCIITDSQT 60
 QY 61 SDPRLEWKIKQDEQTYVFPFNKIQDLAGRAEILGKTSIKWNTRDSALYRCVVAR 120
 DB 61 SDPRLEWKIKQDEQTYVFPFNKIQDLAGRTDVFGLSLRWNTSDSALYRCVVAL 120
 QY 121 NDRKEIDEIVLTQVQKPVTPVCRVPAVPVGRMATLHCESEGHPRPHYSWYRNDVPL 180
 DB 121 NDRKEVDEITIELIVQVQKPVTPVCRIPAAVPVGRMATLHCESEGVPRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYICIASNDAGSARCEQDMEVDL 240
 DB 181 PTDSRANPRFQNSPHVNSSETGLVFNVAHVHKDDSGQYICIASNDAGAACRCEQDMEVDL 240
 QY 241 NIGGIIGVVLVAVLALITLIGCCAYRGGYFINKKDGESYKNPKGPGVNYIRTDEG 300
 DB 241 NIAGIIGVVLVAVLITMGIICAYRGCFTISSKQDGESYKSPKHGDGVNYIRTSEG 300
 QY 301 DFRHKSSPVI 310
 DB 301 DFRHKSSPVI 310

RESULT 6

Q9D1M9
 ID Q9D1M9 PRELIMINARY; PRT; 310 AA.
 AC Q9D1M9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 1110002N23Rik protein.
 OS JCAM3 OR JCAM2 OR 1110002N23RIK.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=2108560; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ribgwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690 (2001).
 DR EMBL; AK003326; BAB22715.1; -;
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig_2.
 DR SMART; SM00408; Igc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 86.2%; Score 1411; DB 11; Length 310;
 Best Local Similarity 85.5%; Pred. No. 8.2e-131;
 Matches 265; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

QY 1 MALRPPRLRLCARLPDPFLLLFRGCLIGAVNLKSSNRPVQPFESVELSCIITDSQT 60
 DB 1 MALSRRLRLRLYARLPDPFLLLFRGCLIGAVNLKSSNRPVQPFESVELSCIITDSQT 60
 QY 61 SDPRLEWKIKQDEQTYVFPFNKIQDLAGRAEILGKTSIKWNTRDSALYRCVVAR 120
 DB 61 SDPRLEWKIKQDEQTYVFPFNKIQDLAGRTDVFGLSLRWNTSDSALYRCVVAL 120
 QY 121 NDRKEIDEIVLTQVQKPVTPVCRVPAVPVGRMATLHCESEGHPRPHYSWYRNDVPL 180
 DB 121 NDRKEVDEITIELIVQVQKPVTPVCRIPAAVPVGRMATLHCESEGVPRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYICIASNDAGSARCEQDMEVDL 240
 DB 181 PTDSRANPRFQNSPHVNSSETGLVFNVAHVHKDDSGQYICIASNDAGAACRCEQDMEVDL 240
 QY 241 NIGGIIGVVLVAVLALITLIGCCAYRGGYFINKKDGESYKNPKGPGVNYIRTDEG 300
 DB 241 NIAGIIGVVLVAVLITMGIICAYRGCFTISSKQDGESYKSPKHGDGVNYIRTSEG 300
 QY 301 DFRHKSSPVI 310
 DB 301 DFRHKSSPVI 310

RESULT 7
 Q9J159
 ID Q9J159 PRELIMINARY; PRT; 298 AA.
 AC Q9J159;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Vascular endothelial junction-associated molecule (junctional adhesion
 molecule-3) (2410030G21Rik protein).
 OS JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21RIK.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6J; PubMed=10779521;
RA MEDLINE=20317114; PubMed=10779521;
RX Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT the Immunoglobulin Superfamily, Is Localized to Intercellular
RT Boundaries of Endothelial Cells.";
RL J. Biol. Chem. 275:19139-19145(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP PubMed=11036763;
RX Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RA "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AF255911; AAF81224.1; -
DR EMBL; AJ291757; CAC20699.1; -
DR EMBL; AK013914; BAB29053.1; -
DR EMBL; AK010616; BAB27064.1; -
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_2.
DR PROSITE; PS0835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 33047 MW; 1124E0F07B6CF751 CRC64;

Query Match 29.7%; Score 486.5; DB 11; Length 298;
Best Local Similarity 36.7%; Pred. No. 1.7e-39;
Matches 114; Conservative 54; Mismatches 116; Indels 27; Gaps 9;

QY 13 ARLPDFLLFRGLGAVNLKSN-----RTPVQEFSEVLSCLITDSQSDP 63
DB 2 ARSPQGLMLLLHYLVALDYHKANGFSASKDHQEVTVIEFQRAILAC-KTPKKTSS 60
QY 64 RIEWKKIQDEQTVVFFDNKIQGLAGRAEILGKTSKIMNVRDSDSALYRCEVVARND 123
DB 61 RLEWKV-GQGVSLVYQQALQGDQFDRAEI-DFNIRIKNVRSDAGEYRCEVSAPTEQ 118
QY 124 -KEIDEIVIELTVQVKPTVPCRVKAVPVGMATLHCQSEGHPRPHYSWYRNDVPLPT 182
DB 119 QQNLEQKVMLEVLVAPVACEVPTSVMTGSVVELRCQDKEGNPAPEYINFKDGHSL-- 176
QY 183 DSRANPRF---NRSFHLNSETGLVFTAVHKDSDGQYCIASNDAGSARCEQMEYVD 239
DB 177 --LGNPKRGTHNSSYTNTKSGILQFNMI SKDSDGYYCEARNVGHRRCPGKMQVDV 234
QY 124 -KEIDEIVIELTVQVKPTVPCRVKAVPVGMATLHCQSEGHPRPHYSWYRNDVPLPT 182
DB 119 QQNLEQKVMLEVLVAPVACEVPTSVMTGSVVELRCQDKEGNPAPEYINFKDGHSL-- 176
QY 183 DSRANPRF---NRSFHLNSETGLVFTAVHKDSDGQYCIASNDAGSARCEQMEYVD 239
DB 177 --LGNPKRGTHNSSYTNTKSGILQFNMI SKDSDGYYCEARNVGHRRCPGKMQVDV 234
QY 240 LNIIGIIGVLVAVLALITLIGICAVRRGVFINNKQDGESYKPKGPDGVNIRITDEE 299
DB 235 LNIIGIATVVVAVFVSVGLGTCYAKRGYF-----SKETSFOKQSP--ASKYTTMSE 287
QY 300 GDFRHKSSFVI 310

DB 288 NDFKHTKSFII 298
RESULT 8
QY 08C5K9 PRELIMINARY; PRT; 298 AA.
AC 08C5K9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Junction cell adhesion molecule 2.
GN JAM2 OR JCAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK078128; BAC37139.1; -
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 33182 MW; 1131F0BF089CBB51 CRC64;

Query Match 29.7%; Score 486.5; DB 11; Length 298;
Best Local Similarity 37.0%; Pred. No. 1.7e-39;
Matches 115; Conservative 54; Mismatches 115; Indels 27; Gaps 9;

QY 13 ARLPDFLLFRGLGAVNLKSN-----RTPVQEFSEVLSCLITDSQSDP 63
DB 2 ARSPQGLMLLLHYLVALDYHKANGFSASKDHQEVTVIEFQRAILAC-KTPKKTSS 60
QY 64 RIEWKKIQDEQTVVFFDNKIQGLAGRAEILGKTSKIMNVRDSDSALYRCEVVARND 123
DB 61 RLEWKV-GQGVSLVYQQALQGDQFDRAEI-DFNIRIKNVRSDAGEYRCEVSAPTEQ 118
QY 124 -KEIDEIVIELTVQVKPTVPCRVKAVPVGMATLHCQSEGHPRPHYSWYRNDVPLPT 182
DB 119 QQNLEQKVMLEVLVAPVACEVPTSVMTGSVVELRCQDKEGNPAPEYINFKDGHSL-- 176
QY 183 DSRANPRF---NRSFHLNSETGLVFTAVHKDSDGQYCIASNDAGSARCEQMEYVD 239
DB 177 --LGNPKRGTHNSSYTNTKSGILQFNMI SKDSDGYYCEARNVGHRRCPGKMQVDV 234
QY 240 LNIIGIIGVLVAVLALITLIGICAVRRGVFINNKQDGESYKPKGPDGVNIRITDEE 299
DB 235 LNIIGIATVVVAVFVSVGLGTCYAKRGYF-----SKETSFOKQSP--ASKYTTMSE 287
QY 300 GDFRHKSSFVI 310
DB 288 NDFKHTKSFII 298

RESULT 9
QY 08CB95 PRELIMINARY; PRT; 298 AA.
AC 08CB95;
DT 01-MAR-2003 (TRENBLrel. 23, Created)


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Qy 83 KIQDLAGRAHILKTSKINWTRDSALYRCVAVNRDRKDEIVIELTVQKPTP 142
Db 77 SLTAPYKDR-IPYPOGITLQITRKDAGEYSCVTSTGSKTYCEAKIQLVAFSPK 135
Qy 143 VCRYPKAPVCKMATLHCOSEGEHPRPHYSWYRNDVPLPTDSRANPRFRNSPFLNGSTG 202
Db 136 VAQVPRSVSTGSVAELLCVENDGYPPTFIWRNKSFM-----QIAP--QNSTYIIDPKTG 189
Qy 203 TLVFTAVHKDDSGQYCIASHNAGSARCEBQEMEVYDINIGIIGGVLLVLAIALITLG 262
Db 190 VLKFAAVSTSDSGEYCEATNQKQASDLVRMDVDVNVGGIVAAVIVLLIALLIGFG 249
Qy 263 ICCAYRGYFINNKODGESYKPKPGDVNIRTDDEGDPRHKSFPVI 310
Db 250 MWFAYSRGYLDKRNKKVIYSLPSE-----TRSDKNFOOTSFLV 289

RESULT 12
Q8VC39 Q8VC39 PRELIMINARY; PRT; 300 AA.
AC Q8VC39;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (function cell adhesion molecule1).
GN FHLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; BC021876; AAH21876.1; --
DR EMBL; AK033574; BAC28369.1; --
DR MGD; MGI:1321398; FHLR.
DR GO; GO:0005515; F:protein binding, IPI.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein_
SQ SEQUENCE 300 AA; 32423 MW; 3CE561B8FF3B97EC CRC64;

Query Match 27.9%; Score 457.5; DB 11; Length 300;
Best Local Similarity 35.6%; Pred. No. 1.3e-36;
Matches 106; Conservative 56; Mismatches 121; Indels 15; Gaps 7;

Qy 20 LLLFRGLIGAV-----NLKSSNRTPVQBFSEVLSCLITDSQTSDPRIEWKIQDEQ 74
Db 11 LLFLFTSMILGQKGSVVYTAQSDVQVPENESIKLTC--TYSGFSSPRVWFVQGST 68

Qy 75 TTVYFPDKIQGLAGRAEILKTSKINWTRDSALYRCVAVNRDRKDEIVIELT 134
Db 69 TALVCTNSQITAPYADRV-TFSSSGITFSSVTRKNGEYTC-MWSEGGQNYGEVSHLT 126

Qy 135 VQVKPTVPVCRVPKAVPVGKMATLHCOSEGEHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
Db 127 LVVPPSKPTISVSSVTIGNRAVLTCSEHDSGPSPEYSWPKDGISMLTADAKTRAFNWS 186

Qy 194 SFHNSGTGLVFTAVHKDDSGQYCIASHNAGSARCEBQEMEVYDINIGIIGGVLLV 252
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Db 187 SFTIDPKSGDILFPVTFAPDSGEYTCQAGNGVGTNRSEARMNDVAVELNGVIVRAVLT 246
Qy 253 LAVLALITLGICCAYRGYFINNKODGESYKPKPGDVNIRTDDEGDPRHKSFPVI 310
Db 247 LILGLLIFGVWFAYSRGYFERTKKG-----TAPGKKVIYSQPSRSEGBFKQTSFLV 300

RESULT 13
Q7SVQ7 Q7SVQ7 PRELIMINARY; PRT; 300 AA.
AC Q7SVQ7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054305; AAH54305.1; --
KW Hypothetical protein.
FT NON-TER
SQ SEQUENCE 300 AA; 32858 MW; 02BC49DC74E271D4 CRC64;

Query Match 26.9%; Score 440.5; DB 13; Length 300;
Best Local Similarity 34.7%; Pred. No. 6.2e-35;
Matches 103; Conservative 55; Mismatches 114; Indels 25; Gaps 7;

Qy 20 LLLFRGLIGA--VNLKSSNRTPVQBFSEVLSCLITDSQTSDP--PRIEWKI-QDE 73
Db 23 LALLCCCLTAALAGVATPDPTITVKEGSDPLRC-----SYTSDYINPRVWFVFNKQD 78

Qy 74 QTTVFPDKIQGLAGRAEILKTSKINWTRDSALYRCVAVNRDRKDEIVIEL 133
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Db 79 ETSFVFDGSLTASYKDRATSTPQ-GIKLNQVTRKDGSEYCEVSTSTGKVLVYGEAKIQ 137
Qy 134 TVQKPEVTPVCRVPAVPGVGMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPRFRNS 193
Db 138 QVIVAPGTBVAQVPSSARTSGVAELMCVETQGFPLPTFTWHNNSPMQAKS-----QNS 191
Qy 194 SFLHNSGTGLVFTAVHKDDSGOYCIASNDAGSARCEBQEMEVYDLNIGGLIGVLVVL 253
Db 192 TTYIDNTGVLFASFVGTSDSGEYCKATNSQEQSSAIVRMDVDVNVGGIVAAVVIL 251
Qy 254 AVLALITLIGICAYRGYFINNKQGESYKPKDPGVNYIRTDSEGDPRHKSFPVI 310
Db 252 LILALLGFLWFAYSRYGLDRKGNKKVYQSPE-----TRSDKNEQQTSSFLV 300
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RESULT 14

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Q9Y5B2 PRELIMINARY; PRT; 259 AA.
AC Q9Y5B2;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Junction adhesion molecule.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Nusrat A., Schnell F.J., Walsh S., Reeves T.A., Pochet M.,
RA Foley C., Farkos C.A.;
RT "Human junctional adhesion molecule is expressed by polarized columnar
RT epithelia and regulates tight junction resealing.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154005; AAD43794.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 259 AA; 28122 MW; FE38521A911582D0 CRC64;
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Query Match 20.5%; Score 336; DB 4; Length 259;
Best Local Similarity 29.6%; Pred. No. 1.1e-24;
Matches 81; Conservative 45; Mismatches 110; Indels 38; Gaps 7;

Qy 42 VVQEPESVLSCLITSDQSDPRIENWKIQDEQTTVFFDNKIQDLAGRABILGKTSLK 101
Db 19 ILPENNPPVLSKAY--SGFSRPR---AASYEDRVTFI-----PTGIT 55

Qy 102 IKNVTRDSALYRCEVVVARNDREIDIEIVIELTVQVKPVPVCRVPAVPGVGMATLHCQ 161
Db 56 FKSVTREDTCTTTC-WVFEGGNSYGEVKVLIVLPVPPSKPTVNIPISSATIGNRAVLTC 114

Qy 162 ESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSFLHNSGTGLVFTAVHKDDSGOYCI 221
Db 115 EQDGPSPSEYTFWPKDGMVPTNPKRAPSNSVSNVLPNPTGRLVFPDPLSADTGRYSCE 174

Qy 222 SNDAGSARCEQ-EMEVYDLNIGGLIGVLVLAVALITLIGICAYRGYFINNKQDGE 280
Db 175 RNYGTYGFTMSNVRMEAVRNVGVVAAVLVLILIGLIFVFIWFAYSRGHFORTKKGTS 234

Qy 281 S-----YKNPGKPDGVNYIRTDSEGDPRHKSFPVI 310
Db 235 SKKVIYQSPS-----ARSEGEFKQTSFLV 259
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RESULT 15

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Q9UKD5 PRELIMINARY; PRT; 173 AA.
ID Q9UKD5
AC Q9UKD5;
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DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirsch T., Wellner M., Haller H., Lippoldt A.;
RT "Cloning of the rat junctional adhesion molecule (JAM).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241261; AAP61729.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 173 AA; 18706 MW; 3EE3ECDFA5AFB8B2 CRC64;

Query Match 19.9%; Score 326; DB 11; Length 173;
Best Local Similarity 40.3%; Pred. No. 6.1e-24;
Matches 71; Conservative 28; Mismatches 71; Indels 6; Gaps 3;

Qy 137 VKPVPVCRVPAVPGVGMATLHCQSEGHPRPHYSWYRNDVPLPTDSRANPRFRNSP 195
Db 2 VPPSKPTVSPSSVTIGNRAVLTCSEHDGSPPSSEYWFKDGVPMLTADAKKTRAFINSS 61

Qy 196 HLNSETGLVFTAVHKDDSGOYCIASNDAGSA-RCEQEMEVYDLNIGGLIGVLVLA 254
Db 62 TIDPKSGDLVFDVPSAFDSGYYICRAQNGYGTANRSEAVRMEAVELNVGGIVAAVLTLI 121

Qy 255 VLALITLIGICAYRGYFINNKQGESYKPKDPGVNYIRTDSEGDPRHKSFPVI 310
Db 122 LLGLLIPGIWFAYSRGYFERTKKG----TAPGKKVIYQSPSARSEGEFKQTSFLV 173
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Search completed: June 15, 2004, 11:05:06
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:01:19 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MAURRPPRLRCARLPDFL.....VNYRTDEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgm2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgm2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1637	100.0	310	4	US-09-907-794A-423
2	1637	100.0	310	4	US-09-905-125A-423
3	1637	100.0	310	4	US-09-902-775A-423
4	481	29.4	298	4	US-09-152-060-76
5	461.5	28.2	312	4	US-09-254-465A-9
6	461.5	28.2	312	4	US-09-907-794A-64
7	461.5	28.2	312	4	US-09-905-125A-64
8	461.5	28.2	312	4	US-09-902-775A-64
9	457.5	27.9	300	4	US-09-254-465A-10
10	424	25.9	299	3	US-09-188-930-331
11	424	25.9	299	4	US-09-462-270-2
12	424	25.9	299	4	US-09-254-465A-1
13	424	25.9	299	4	US-09-312-283C-189
14	424	25.9	299	4	US-09-312-283C-331
15	424	25.9	299	4	US-09-907-794A-119
16	424	25.9	299	4	US-09-905-125A-119
17	424	25.9	299	4	US-09-902-775A-119
18	412	25.2	299	3	US-09-188-930-189
19	392.5	24.0	260	4	US-09-254-465A-23
20	392.5	24.0	263	4	US-09-254-465A-25
21	288	17.6	205	1	US-09-462-270-4
22	228.5	14.0	319	4	US-08-597-495B-22
23	228.5	14.0	319	3	US-09-068-051A-22
24	228.5	14.0	319	4	US-09-336-536-67
25	228.5	14.0	319	4	US-09-254-465A-6
26	217.5	13.3	270	4	US-09-254-465A-24
27	217.5	13.3	273	4	US-09-254-465A-26

28	215.5	13.2	318	3	US-09-068-051A-32	Sequence 32, Appl
29	197.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appl
30	173.5	10.6	370	4	US-09-336-536-28	Sequence 28, Appl
31	171.5	10.5	394	4	US-09-336-536-39	Sequence 39, Appl
32	169.5	10.4	390	2	US-08-979-424-1	Sequence 1, Appl
33	169.5	10.4	390	4	US-09-907-794A-39	Sequence 39, Appl
34	169.5	10.4	390	4	US-09-905-125A-39	Sequence 39, Appl
35	169.5	10.4	390	4	US-09-902-775A-39	Sequence 39, Appl
36	167	10.2	365	4	US-09-336-536-40	Sequence 29, Appl
37	166.5	10.2	341	4	US-09-336-536-29	Sequence 29, Appl
38	163.5	10.0	398	4	US-09-778-510-6	Sequence 6, Appl
39	163.5	10.0	398	4	US-09-907-794A-84	Sequence 84, Appl
40	163.5	10.0	398	4	US-09-905-125A-84	Sequence 84, Appl
41	163.5	10.0	398	4	US-09-902-775A-84	Sequence 31, Appl
42	162.5	9.9	246	4	US-09-336-536-31	Sequence 4, Appl
43	161	9.8	313	4	US-09-700-397-4	Sequence 3, Appl
44	161	9.8	344	4	US-09-700-397-3	Sequence 2, Appl
45	160.5	9.8	365	3	US-08-928-383B-2	

ALIGNMENTS

RESULT 1

US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNTPVVOEPESVLSCTIIDSQT 60
DB 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNTPVVOEPESVLSCTIIDSQT 60
QY 61 SDPRIEWKKIQDEQTTVVFNDNKIQDLAGRAILGKTSIKIWNVTRDSALYRCEVVAR 120
DB 61 SDPRIEWKKIQDEQTTVVFNDNKIQDLAGRAILGKTSIKIWNVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNTPVVOEPESVLSCTIIDSQT 60
DB 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNTPVVOEPESVLSCTIIDSQT 60
QY 61 SDPRIEWKKIQDEQTTVVFNDNKIQDLAGRAILGKTSIKIWNVTRDSALYRCEVVAR 120
DB 61 SDPRIEWKKIQDEQTTVVFNDNKIQDLAGRAILGKTSIKIWNVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180


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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76

Query Match      29.4%; Score 481; DB 4; Length 298;
Best Local Similarity 35.8%; Pred. No. 7.7e-41;
Matches 114; Conservative 60; Mismatches 116; Indels 28; Gaps 10;

QY 1 MALRPPRLRLCARLPDPFLLLRGCLIG-----AVNLKSSNRTPVQ--BPESVELSC 53
DB 1 MARRSRRL-----LLLLRYLVVALGVKAYGFSAPKQDQOVVAVYQAILAC 50

QY 54 ITTDSQTSPIRLEWKIODEQTYVFFDNKIQDLAGRAEILGKTSKIKWVTRDSALY 113
DB 51 -KTPKKTYSRLWKKL-GRSVSPVYQOTLQDGFNRAEMI-DFNIRIKNVTRSDAGKY 107

QY 114 RCEVVARNDR-KEIDRIVIELTVQKVPVPCRVKAVPVGMATHLCOBSEGHPRPHYS 172
DB 108 RCEVSAPSEQGNLEBDVTLEVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

QY 173 WYRNDVPLTDSRANPRFNSSPHLNSGTGLVETAVHKDDSGQYVCIASNDAGSARCEE 232
DB 168 WPKGIRLLENRLGSSQTSNSTYTNKTKGTQFNTVSKLDGYSCEARNVSVYRCPG 227

QY 233 QMEVYDNLGIGIIGVLVLAVALITLIGICAVRGGYF 272
DB 228 KEMQVDDNLISGLIAAVVVALVISVGLGVCAQRKGYF 267

QY 293 YIRTEGDFRHKSSPVI 310
DB 281 KATTMSENDFKTKSPII 298

RESULT 5
US-09-254-465A-9
; Sequence 9, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 9
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-9

Query Match      28.2%; Score 461.5; DB 4; Length 312;
Best Local Similarity 37.1%; Pred. No. 8.1e-39;
Matches 104; Conservative 52; Mismatches 103; Indels 21; Gaps 7;

QY 1 MALRPPRLRLCARLPDPFLLLRGCLIG-----AVNLKSSNRTPVQ--BPESVELSC 53
DB 1 MARRSRRL-----LLLLRYLVVALGVKAYGFSAPKQDQOVVAVYQAILAC 50

QY 54 ITTDSQTSPIRLEWKIODEQTYVFFDNKIQDLAGRAEILGKTSKIKWVTRDSALY 113
DB 51 -KTPKKTYSRLWKKL-GRSVSPVYQOTLQDGFNRAEMI-DFNIRIKNVTRSDAGKY 107

QY 114 RCEVVARNDR-KEIDRIVIELTVQKVPVPCRVKAVPVGMATHLCOBSEGHPRPHYS 172
DB 108 RCEVSAPSEQGNLEBDVTLEVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

QY 173 WYRNDVPLTDSRANPRFNSSPHLNSGTGLVETAVHKDDSGQYVCIASNDAGSARCEE 232
DB 168 WPKGIRLLENRLGSSQTSNSTYTNKTKGTQFNTVSKLDGYSCEARNVSVYRCPG 227

QY 233 QMEVYDNLGIGIIGVLVLAVALITLIGICAVRGGYF 272
DB 228 KEMQVDDNLISGLIAAVVVALVISVGLGVCAQRKGYF 267

RESULT 6
US-09-707-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijav, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
```

APPLICANT: Pong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-794A-64

Query Match 28.2%; Score 461.5; DB 4; Length 312;
Best Local Similarity 37.1%; Pred. No. 8.1e-39;
Matches 104; Conservative 52; Mismatches 103; Indels 21; Gaps 7;

QY 1 MALRRPRLRLCARLPDFLLLLFRGLIG-----AVNLKSSNRTPVVO--EFESVELSC 53
DB 1 MARSRHRL-----LLLLLYLVVALGYHAYGFSAPKQOQVTVAVETQAILAC 50
QY 54 IITDSQSDPRIEWKIQDEQTYVFFDNKIQGDLAGRAEILGKTSLKINWVTRDSALY 113
DB 51 -KTPKTVSSRLWKLL-GRSVSFYVYQOTLQEDFKNAEMI-DFNIRIKNVTSDAGKY 107
QY 114 RCEVARNDR-KBIDEIVIELTVQVKTPTVPCRVKAVPVGMATLHCQESGHPHYS 172
DB 108 RCEVSAPSEQQNLIEDTVTLEVLVAPAVPSCEVPSSALSGTVVRLCQDKGNPAPEYT 167
QY 173 WYRNDVPLTDSRANPRFNSFLHNSGTGLVFTAVHKDSQGYVCIASNDAGSARCEB 232
DB 168 WFKGIRLEPLRGSQSTNSYNTWTKTGLQFNTVSKLDGYSCEARNVGYTRCPG 227
QY 233 QMEVYDNLIGIGGLVWLAVLALITLIGICAVRRGYF 272
DB 228 KRMQVDDLNLISGLIAVAVVVALVISVCGLVGYAQKGYF 267

RESULT 7
US-09-905-125A-64
Sequence 64, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen

Query Match 28.2%; Score 461.5; DB 4; Length 312;
Best Local Similarity 37.1%; Pred. No. 8.1e-39;
Matches 104; Conservative 52; Mismatches 103; Indels 21; Gaps 7;
QY 1 MALRRPRLRLCARLPDFLLLLFRGLIG-----AVNLKSSNRTPVVO--EFESVELSC 53
DB 1 MARSRHRL-----LLLLLYLVVALGYHAYGFSAPKQOQVTVAVETQAILAC 50
QY 54 IITDSQSDPRIEWKIQDEQTYVFFDNKIQGDLAGRAEILGKTSLKINWVTRDSALY 113

Db 51 -KTPKKTSSRLWKGL-GRSVFVYQQTQGGDFKRAEMI-DFNIRIKNVTSDAGKY 107
Qy 114 RCEVVARNDR-KEIDRIVIELTVQVVKPTVPCVRKPAVPGKMATLHCQESGEGHPRPHYS 172
Db 108 RCEVSAPSEQQLNEEDVTTLLEVLVAPAVPSCVEPSSALSGTVVLRQCKEGNPAPEYT 167
Qy 173 WYRNDVPLTDSRANPRFRNSFHLNSETGLVFTAVHKDSCGYCYCIASNDAGSARCEE 232
Db 168 WFKDGIRLLENPRLGQSQTNSSTYNTKTGTFNTVSKLDTGYSCEARNVSGVRRCPG 227
Qy 233 QMEVYDLNIGGIIGVLVLAVALITLIGICCAVRGGYF 272
Db 228 KRMQVDDLNISGIIIAAVVVALVISVCGLVGYCAQRKGYP 267

RESULT 8

US-09-902-775A-64

; Sequence 64, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-64

Query Match 28.2%; Score 461.5; DB 4; Length 312;
Best Local Similarity 37.1%; Fred. No. 8.1e-39;
Matches 104; Conservative 52; Mismatches 103; Indels 21; Gaps 7;

Qy 1 MALRRPRLRLCARLPDPFLLLPGLIG-----AVNLKSSNRTPVVO--BFSVSLSC 53
Db 1 MARRSRRL-----LLLLLRYLVVALGYHKAYGFSAPKQQQVTVAVEQAILAC 50
Qy 54 IITDSQTSDPRIEWKIQDEQTVVFPDNKIQGLAGRAELIGKTSLKINVTTRDSALY 113
Db 51 -KTPKKTSSRLWKGL-GRSVFVYQQTQGGDFKRAEMI-DFNIRIKNVTSDAGKY 107
Qy 114 RCEVVARNDR-KEIDRIVIELTVQVVKPTVPCVRKPAVPGKMATLHCQESGEGHPRPHYS 172
Db 108 RCEVSAPSEQQLNEEDVTTLLEVLVAPAVPSCVEPSSALSGTVVLRQCKEGNPAPEYT 167
Qy 173 WYRNDVPLTDSRANPRFRNSFHLNSETGLVFTAVHKDSCGYCYCIASNDAGSARCEE 232
Db 168 WFKDGIRLLENPRLGQSQTNSSTYNTKTGTFNTVSKLDTGYSCEARNVSGVRRCPG 227
Qy 233 QMEVYDLNIGGIIGVLVLAVALITLIGICCAVRGGYF 272
Db 228 KRMQVDDLNISGIIIAAVVVALVISVCGLVGYCAQRKGYP 267

RESULT 9

US-09-254-465A-10
; Sequence 10, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 10
; LENGTH: 300


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; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 1
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-1

Query Match      25.9%; Score 424; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 5.1e-35;
Matches 101; Conservative 48; Mismatches 137; Indels 22; Gaps 7;

QY      8 RRLRCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIIITDSQTSDPRIEW 67
DB      9 RKLLCL-----FLAILLCSLALSGVTVHSSEPEVRIPENNPVKLSLAY--SGFSSPRVW 62

QY      68 KKIODEQTTYYVFFDNKIQDLAGRAEILGKTSKIWNVTRRDSALYRCVAVARNDRKID 127
DB      63 KPDQDGTTRLVCYNNKKTASYEDRVTFLL-PTGITPKSVTREDTGTTC-MVSEEGNSYG 120

QY      128 EIVIELTVQVKPVPVCRVPAVPGVKMATLHCQSEBGPSPHYSHYRNDVPLPTDSRAN 187
DB      121 EVKVKLIVLVPPSKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTWFKDGIWMTNPKST 180

QY      188 PRFRNSSPHLNSGTGLVFTAVHKDDSGQYCIASNDAGSARCEQ-EHEVVDLNTGGII 246
DB      181 RAPSNSYVLNPTTGELVFDPLSADTGEYSCEARNGYGTPTMTSNAVRMEAVERNVGVIV 240

QY      247 GGVLVAVLALITLIGICCAVYRGYFINNKQDGS-----YKNPGKPDGVNYIRTDSEGDF 302
DB      241 AAVLVTLILGLVFGIWFAYSRGHFDRTKGTSSKKVIYSQPS-----ARSEGEF 291

QY      303 RHKSSFVI 310
DB      292 KQTSSFLV 299

RESULT 14
US-09-312-283C-331
; Sequence 331, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-331

Query Match      25.9%; Score 424; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 5.1e-35;
Matches 101; Conservative 48; Mismatches 137; Indels 22; Gaps 7;

QY      8 RRLRCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIIITDSQTSDPRIEW 67
DB      9 RKLLCL-----FLAILLCSLALSGVTVHSSEPEVRIPENNPVKLSLAY--SGFSSPRVW 62

QY      68 KKIODEQTTYYVFFDNKIQDLAGRAEILGKTSKIWNVTRRDSALYRCVAVARNDRKID 127
DB      63 KPDQDGTTRLVCYNNKKTASYEDRVTFLL-PTGITPKSVTREDTGTTC-MVSEEGNSYG 120

QY      128 EIVIELTVQVKPVPVCRVPAVPGVKMATLHCQSEBGPSPHYSHYRNDVPLPTDSRAN 187
DB      121 EVKVKLIVLVPPSKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTWFKDGIWMTNPKST 180

QY      188 PRFRNSSPHLNSGTGLVFTAVHKDDSGQYCIASNDAGSARCEQ-EHEVVDLNTGGII 246
DB      181 RAPSNSYVLNPTTGELVFDPLSADTGEYSCEARNGYGTPTMTSNAVRMEAVERNVGVIV 240

QY      247 GGVLVAVLALITLIGICCAVYRGYFINNKQDGS-----YKNPGKPDGVNYIRTDSEGDF 302
DB      241 AAVLVTLILGLVFGIWFAYSRGHFDRTKGTSSKKVIYSQPS-----ARSEGEF 291

Query Match      25.9%; Score 424; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 5.1e-35;
Matches 101; Conservative 48; Mismatches 137; Indels 22; Gaps 7;

QY      8 RRLRCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIIITDSQTSDPRIEW 67
DB      9 RKLLCL-----FLAILLCSLALSGVTVHSSEPEVRIPENNPVKLSLAY--SGFSSPRVW 62

QY      68 KKIODEQTTYYVFFDNKIQDLAGRAEILGKTSKIWNVTRRDSALYRCVAVARNDRKID 127
DB      63 KPDQDGTTRLVCYNNKKTASYEDRVTFLL-PTGITPKSVTREDTGTTC-MVSEEGNSYG 120

QY      128 EIVIELTVQVKPVPVCRVPAVPGVKMATLHCQSEBGPSPHYSHYRNDVPLPTDSRAN 187
DB      121 EVKVKLIVLVPPSKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTWFKDGIWMTNPKST 180

QY      188 PRFRNSSPHLNSGTGLVFTAVHKDDSGQYCIASNDAGSARCEQ-EHEVVDLNTGGII 246
DB      181 RAPSNSYVLNPTTGELVFDPLSADTGEYSCEARNGYGTPTMTSNAVRMEAVERNVGVIV 240

QY      247 GGVLVAVLALITLIGICCAVYRGYFINNKQDGS-----YKNPGKPDGVNYIRTDSEGDF 302
DB      241 AAVLVTLILGLVFGIWFAYSRGHFDRTKGTSSKKVIYSQPS-----ARSEGEF 291
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Db 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKGTSSKKVIYSQPS-----ARSEGEF 291

Qy 303 RHKSSEFVI 310

Db 292 KQTSSFLV 299

RESULT 15

US-09-907-794A-119

Sequence 119, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary B.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mathet, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

PRIOR FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 119

LENGTH: 299

TYPE: PRT

ORGANISM: Homo sapiens

US-09-907-794A-119

Query Match 25.9%; Score 424; DB 4; Length 299;

Best Local Similarity 32.8%; Pred No. 5.1e-35;

Matches 101; Conservative 48; Mismatches 137; Indels 22; Gaps 7;

Qy 8 RLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVOBFSEVLSLIIITDSQTSQSPRIEW 67

Db 9 RKLCLL---FILAILLCSLALGSVTVHSSBPEVRIPENNPKLSLAY--SGFSSPRVEM 62

Qy 68 KKIQDEQTYTFYFDNKKIQGDLGRAEILGKTSLKIMVWTRDSALYRCVAVNRDKRID 127

Db 63 KFDQGDTRLVYCNKKITASYEDRVTFPL-PTGITFKSVTRDVTGTYTC-MVSEEGNSVG 120

Qy 128 BIVIELTVQVKPVPVCKRPAVPVGMATLHCBSBGRPHRPHYSWYRNDVPLTDSRAN 187

Db 121 EVKVLVLVLPSPKPTVNPSSATIGNRAVLTCSQDGPSPSEYTWPKDGIWPTNPKST 180

Qy 188 PRFRNSFHLNSBTGLVFTAVHKDDSQYYCIAANDAGSARCEBQ-EMEVYDLNIGGI 246

Db 181 RAFNSSVVLNPTTGLVFDPLSASDTGEYSCEARNGYGTPTMTSNAVRMEAVERNVGVIV 240

Qy 247 GGVLVVLAVLALITLGICCAVRCGYFINNKQDGS-----YKNPGKPDGVNYIRTDEGDP 302

Db 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKGTSSKKVIYSQPS-----ARSEGEF 291

Qy 303 RHKSSEFVI 310

Db 292 KQTSSFLV 299

Search completed: June 15, 2004, 11:06:32

Job time : 17.5 secs

PCT/US99/28313

~~2003224~~

20032221

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 10:50:54 ; Search time 51.5 Seconds
(without alignments)
1700.771 Million cell updates/sec

Title: US-09-524-531C-15

Perfect score: 1637

Sequence: 1 MALRRPRLRLCARLPDFL.....VNYRTDEGDFRHKSSFVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1637	100.0	310	3 AAY96735	Aay96735 PRO1868,
2	1637	100.0	310	3 AAB33457	Aab33457 Human PRO
3	1637	100.0	310	3 AAB27276	Aab27276 Human con
4	1637	100.0	310	4 AAB80272	Aab80272 Human PRO
5	1637	100.0	310	4 AAM93905	Aam93905 Human pol
6	1637	100.0	310	4 AAM93323	Aam93323 Human pol
7	1637	100.0	310	4 AAU12440	Aau12440 Human PRO
8	1637	100.0	310	4 AAB80383	Aab80383 Secreted
9	1637	100.0	310	4 AAB80408	Aab80408 Secreted
10	1637	100.0	310	4 AAB80409	Aab80409 Secreted
11	1637	100.0	310	5 ABG92709	Abg92709 Human sec
12	1637	100.0	310	5 ABG91361	Abg91361 Novel hum
13	1637	100.0	310	5 ABB84947	Abb84947 Human PRO
14	1637	100.0	310	5 ABG65297	Abg65297 Human alb
15	1637	100.0	310	5 ABG65296	Abg65296 Human alb
16	1637	100.0	310	5 ABG65298	Abg65298 Human alb
17	1637	100.0	310	5 ABG31401	Abg31401 Human PRO
18	1637	100.0	310	5 ABB95553	Abb95553 Human ang
19	1637	100.0	310	6 ABU71650	Abu71650 Human PRO
20	1637	100.0	310	6 ABU72377	Abu72377 Novel hum
21	1637	100.0	310	6 ABU80867	Abu80867 Human sec
22	1637	100.0	310	6 ABO17884	Abo17884 Novel hum
23	1637	100.0	310	6 ABU71505	Abu71505 Human PRO
24	1637	100.0	310	6 ADA57610	Ada57610 Human sec
25	1637	100.0	310	6 ADA57611	Ada57611 Human sec

26	1637	100.0	310	6 ADA57309	Ada57309 Human sec
27	1637	100.0	310	6 ABP71277	Abp71277 Human jun
28	1637	100.0	310	6 ABU81138	Abu81138 Human PRO
29	1637	100.0	310	6 ABU71951	Abu71951 Human sec
30	1637	100.0	310	6 ABO01834	Abo01834 Novel hum
31	1637	100.0	310	6 ABU66838	Abu66838 Human PRO
32	1637	100.0	310	6 ABU54407	Abu54407 Human sec
33	1637	100.0	310	6 ABO47422	Abo47422 Human sec
34	1637	100.0	310	6 ABG73314	Abg73314 Human PRO
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36	1637	100.0	310	6 ABO25109	Abo25109 Human sec
37	1637	100.0	310	6 ABU64559	Abu64559 Human sec
38	1637	100.0	310	6 ABU67405	Abu67405 Human sec
39	1637	100.0	310	6 ABO14925	Abo14925 Human sec
40	1637	100.0	310	6 ABU60813	Abu60813 Human sec
41	1637	100.0	310	6 ABU67114	Abu67114 Human sec
42	1637	100.0	310	6 ABU81236	Abu81236 Human PRO
43	1637	100.0	310	6 ABU69682	Abu69682 Novel hum
44	1637	100.0	310	6 ABO14864	Abo14864 Human sec
45	1637	100.0	310	6 ADA46057	Ada46057 Novel hum

ALIGNMENTS

RESULT 1

AAY96735

ID AAY96735 standard; protein; 310 AA.

XX AAY96735;

XX AC AAY96735;

DT 26-SEP-2000 (first entry)

XX DE PRO1868, an A33 antigen homologue.

XX KW PRO1868; A33 antigen; secreted protein; transmembrane protein;

XX KW anti-inflammatory; cytostatic; recombinant production; gene therapy.

XX OS Homo sapiens.

XX FH Key

FT Peptide

FT /label= Signal_peptide

FT Modified-site 26..31

FT /note= "N-myristoylation site"

FT Modified-site 69..77

FT /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 104..107

FT /note= "N-glycosylation site"

FT Modified-site 106..109

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site 107..110

FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 192..195

FT /note= "N-glycosylation site"

FT Modified-site 215..220

FT /note= "N-myristoylation site"

FT Modified-site 226..231

FT /note= "N-myristoylation site"

FT Domain 243..263

FT /label= Transmembrane_domain

FT Modified-site 243..248

FT /note= "N-myristoylation site"

FT Modified-site 244..249

FT /note= "N-myristoylation site"

FT Modified-site 262..267

FT /note= "N-myristoylation site"

FT Modified-site 296..299

FT /note= "Casein kinase II phosphorylation site"

PN WO200036102-A2.

XX

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PD 22-JUN-2000.
XX
PF 01-DEC-1999; 99WO-US028634.
XX
XX 16-DEC-1998; 98US-0112851P.
XX 16-DEC-1998; 98US-0113145P.
XX 22-DEC-1998; 98US-0113511P.
XX 12-JAN-1999; 99US-0115558P.
XX 12-JAN-1999; 99US-0115565P.
XX 12-JAN-1999; 99US-0115733P.
XX 09-FEB-1999; 99US-0119341P.
XX 10-FEB-1999; 99US-0119537P.
XX 12-FEB-1999; 99US-0119965P.
XX 02-JUN-1999; 99WO-US012252.
XX (GETH ) GENENTECH INC.
XX
XX Rotstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
XX WPI; 2000-431586/37.
XX N-PSDB; AAA51265.
XX
XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT transmembrane polypeptide.
XX
XX Claim 1; Fig 14; 154pp; English.
XX
XX This is PRO1868, a putative homologue of A33 antigen, a known colorectal
CC cancer-associated marker. The invention concerns novel secreted and
CC transmembrane proteins, designated PRO polypeptides. The cDNA and gene
CC sequences are useful in the recombinant production of PRO polypeptides,
CC as a hybridization probe to screen libraries to isolate cDNAs with
CC sequence identity to PRO polypeptides or to map the gene encoding the PRO
CC polypeptides and analyzing genetic disorders. The cDNA/gene can also be
CC used to produce transgenic animals useful for the development and
CC screening of therapeutically useful reagents. They can also be used in
CC gene therapy, e.g. to replace a defective gene
XX
XX Sequence 310 AA;
SQ
Query Match 100.0%; Score 1637; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQPFESVELSCIITDSQT 60
QY 61 SDPRIEWKKIQDEQTYVPFDNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCEVVAR 120
DB 61 SDPRIEWKKIQDEQTYVPFDNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCEVVAR 120
QY 121 NDRKIDEIVIELTVQVKDVTVCVRPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
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QY 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEYDL 240
DB 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEVEYDL 240
QY 241 NTGGIIGVVLVAVLALITLIGICCAVRYGYFINNKQDGESYKPKGPGVNYIRDEEG 300
DB 241 NTGGIIGVVLVAVLALITLIGICCAVRYGYFINNKQDGESYKPKGPGVNYIRDEEG 300
QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310
RESULT 2
AAB33457

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ID AAB33457 standard; protein; 310 AA.
XX
AC AAB33457;
XX
XX 29-JAN-2001 (first entry)
XX
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; chryoiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
XX
XX WO200053758-A2.
XX
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005841.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
XX 12-MAR-1999; 99US-0123957P.
XX 23-MAR-1999; 99US-0125775P.
XX 12-APR-1999; 99US-0128849P.
XX 20-APR-1999; 99WO-US008615.
XX 28-APR-1999; 99US-0131445P.
XX 04-MAY-1999; 99US-0132371P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-OCT-1999; 99US-0162506P.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH ) GENENTECH INC.
XX

```

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;
 XX WPI; 2000-572271/53.
 DR N-PSDB; AAC58622.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX Claim 33; Fig 88; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention

XX SQ Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 3; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQEFSEVELSCIITDSQT 60
 Db 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQEFSEVELSCIITDSQT 60
 Qy 61 SDPRIENKKIQDEQTTVFFDNKIQGLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120
 Db 61 SDPRIENKKIQDEQTTVFFDNKIQGLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120
 Qy 121 NDRKEIDETVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
 Db 121 NDRKEIDETVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
 Qy 181 PTDSRANPRFNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEYVDL 240
 Db 181 PTDSRANPRFNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEYVDL 240
 Qy 241 NIGGIIGVLVAVLALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDREG 300
 Db 241 NIGGIIGVLVAVLALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDREG 300
 Qy 301 DFRKSSFVI 310
 Db 301 DFRKSSFVI 310

RESULT 3

AAB27276
 ID AAB27276 standard; protein; 310 AA.

XX AAB27276;

XX 23-FEB-2001 (first entry)

XX Human confluency regulated adhesion molecule 1 #2.

XX

KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
 KW inflammation; cancer; wound; angiogenesis; human;
 KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.

XX Homo sapiens.

XX WO2000053749-A2.

XX 14-SEP-2000.

XX 13-MAR-2000; 2000WO-EP002219.

XX 11-MAR-1999; 99EP-00200746.

XX (RMFD-) RMP DICTAGENE SA.

XX Imhof BA, Aurrand-Lions M;

XX WPI; 2000-587436/55.

XX N-PSDB; AAA95306.

XX Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
 PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
 PT reactions and modulating vascular permeability.

XX Claim 2; Fig 6; 59pp; English.

XX The present sequence is the human confluency regulated adhesion molecule
 CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
 CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
 CC and coding sequence can be used in the treatment of cancer, inflammation,
 CC to modulate cell-cell interactions and angiogenesis, and in the
 CC modulation of wound healing

XX SQ Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 3; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQEFSEVELSCIITDSQT 60
 Db 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQEFSEVELSCIITDSQT 60
 Qy 61 SDPRIENKKIQDEQTTVFFDNKIQGLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120
 Db 61 SDPRIENKKIQDEQTTVFFDNKIQGLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120
 Qy 121 NDRKEIDETVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
 Db 121 NDRKEIDETVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
 Qy 181 PTDSRANPRFNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEYVDL 240
 Db 181 PTDSRANPRFNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEYVDL 240
 Qy 241 NIGGIIGVLVAVLALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDREG 300
 Db 241 NIGGIIGVLVAVLALITLIGICCAVRRGYFINNKQGESYKPKGPDGVNYIRTDREG 300
 Qy 301 DFRKSSFVI 310
 Db 301 DFRKSSFVI 310

RESULT 4

AAB80272
 ID AAB80272 standard; protein; 310 AA.

XX AAB80272;

XX 24-APR-2001 (first entry)

XX DE Human PRO1868 protein.
XX KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiaathmatic; antirheumatic; cancer;
KW antithrilitic; antifertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX OS Homo sapiens.
XX PN WO200104311-A1.
XX PD 18-JAN-2001.
XX PF 22-FEB-2000; 2000WO-US004414.
XX PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX (GETH) GENENTECH INC.
XX AShtenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;
PI Mather JP, Pan J, Faoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2001-081051/09.
DR N-PSDB; AAP72433.
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX Claim 1; Fig 124; 393pp; English.
PS The present sequence is one of sixty one novel secreted and transmembrane
XX PRO polypeptides. The PRO polypeptides are useful for treating skin
CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping
XX Sequence 310 AA;
SQ Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVQBFESVELSCIITDSQT 60

Db 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVQBFESVELSCIITDSQT 60
QY 61 SPRLRMKKIQDEQTYTYPFDNKKIQDLAGRAIILGKTSLKINWVTRDSALYRCEVVAR 120
Db 61 SPRLRMKKIQDEQTYTYPFDNKKIQDLAGRAIILGKTSLKINWVTRDSALYRCEVVAR 120
QY 121 NDRKXIDEIIVLTQVQKFPVTPVCRVPAKVPVGRKMATLHCQSESGHPRPHYSWYRNDVPL 180
Db 121 NDRKXIDEIIVLTQVQKFPVTPVCRVPAKVPVGRKMATLHCQSESGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLNSGTGLVPTAVHKDDSGQYCIASNDAGSARCEOEEMEVYDL 240
Db 181 PTDSRANPRFRNSSPHLNSGTGLVPTAVHKDDSGQYCIASNDAGSARCEOEEMEVYDL 240
QY 241 NIGGIIIGVLVAVLALITLIGICCAIRRGYFINNKQDGESYKNPKGPDGVNIRTDDEG 300
Db 241 NIGGIIIGVLVAVLALITLIGICCAIRRGYFINNKQDGESYKNPKGPDGVNIRTDDEG 300
QY 301 DFRHKSSPVI 310
Db 301 DFRHKSSPVI 310
RESULT 5
ID AAM93905 standard; protein; 310 AA.
XX AAM93905;
XX 06-NOV-2001 (first entry)
XX Human polypeptide, SEQ ID NO: 4051.
XX Human; full length cDNA; cDNA synthesis; oligo-capping.
XX Homo sapiens.
XX BP1130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000EP-00114089.
XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX (HELI-) HELIX RES INST.
PI Ota T, Nishikawa T, Iseogai T, Hayaashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
DR N-PSDB; AAK94867.
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO

XX SQ Sequence 310 AA;
 Query Match 100.0%; Score 1637; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVQBFPSVLSLIIITSQT 60
 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVQBFPSVLSLIIITSQT 60
 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMNVTTRDSALYRCEVVAR 120
 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMNVTTRDSALYRCEVVAR 120
 121 NDRKEIDBIIVELTVQVKPVPFCRVKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180
 121 NDRKEIDBIIVELTVQVKPVPFCRVKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180
 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEQEMEVYDL 240
 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEQEMEVYDL 240
 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKQDGSYKPKPGDGVNYIRTDDEG 300
 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKQDGSYKPKPGDGVNYIRTDDEG 300
 301 DFRHKSSEFI 310
 301 DFRHKSSEFI 310
 RESULT 6
 AAM93323
 ID AAM93323 standard; protein; 310 AA.
 XX AC AAM93323;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide, SEQ ID NO: 2845.
 XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX OS Homo sapiens.
 XX FN EP1130094-A2.
 XX PD 05-SEP-2001.
 XX PP 07-JUL-2000; 2000EP-00114089.
 XX PR 08-JUL-1999; 95JP-00194486.
 XX PR 11-JAN-2000; 2000JP-00118774.
 XX PR 02-MAY-2000; 2000JP-00183765.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WIPI; 2001-524255/58.
 XX DR N-PSDB; AAK94243.
 XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
 XX PT in genetic manipulation.
 XX PS Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
 XX CC The invention relates to primers for synthesizing full length cDNA
 XX CC clones. 830 cDNA molecules encoding a human protein have been isolated
 XX CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 XX CC been determined. Primers for synthesizing the full length cDNA are useful

CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX -SQ Sequence 310 AA;
 Query Match 100.0%; Score 1637; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVQBFPSVLSLIIITSQT 60
 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVQBFPSVLSLIIITSQT 60
 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMNVTTRDSALYRCEVVAR 120
 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMNVTTRDSALYRCEVVAR 120
 121 NDRKEIDBIIVELTVQVKPVPFCRVKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180
 121 NDRKEIDBIIVELTVQVKPVPFCRVKAVPVGMATLHCQESGHPHRYSWYRNDVPL 180
 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEQEMEVYDL 240
 181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEQEMEVYDL 240
 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKQDGSYKPKPGDGVNYIRTDDEG 300
 241 NIGGIIGVLVLAVALITIGICAVRRGYFINNKQDGSYKPKPGDGVNYIRTDDEG 300
 301 DFRHKSSEFI 310
 301 DFRHKSSEFI 310
 RESULT 7
 AAM12440
 ID AAM12440 standard; protein; 310 AA.
 XX AC AAM12440;
 XX DT 24-OCT-2001 (first entry)
 XX DE Human PRO1868 polypeptide sequence.
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 XX KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 XX KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 XX KW A-peptide; factor VIIA; gene therapy.
 XX OS Homo sapiens.
 XX FN WO200140466-A2.
 XX PD 07-JUN-2001.
 XX PP 01-DEC-2000; 2000WO-US032678.
 XX PR 01-DEC-1999; 99WO-US028301.
 XX PR 01-DEC-1999; 99WO-US028634.
 XX PR 02-DEC-1999; 99WO-US028551.
 XX PR 02-DEC-1999; 99WO-US028564.
 XX PR 02-DEC-1999; 99WO-US028565.
 XX PR 09-DEC-1999; 99US-0170262P.
 XX PR 16-DEC-1999; 99WO-US030095.
 XX PR 20-DEC-1999; 99WO-US030911.
 XX PR 20-DEC-1999; 99WO-US030999.
 XX PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US000365.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
 XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21512.
 XX
 PT Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 12; Fig 538; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 310 AA;
 Query Match 100.0%; Score 1637; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7,3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBESVLSCLITDSQT 60
 DB 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBESVLSCLITDSQT 60
 QY 61 SDPRJEWKKIQDBQTTTYVFPDNKIQGLAGRAILGKTSLKINWVTRRDSALYRCEVVAR 120
 DB 61 SDPRJEWKKIQDBQTTTYVFPDNKIQGLAGRAILGKTSLKINWVTRRDSALYRCEVVAR 120
 QY 121 NDRKEIDEITVIELTVQVKFVTPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
 DB 121 NDRKEIDEITVIELTVQVKFVTPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFRNSSPHLNSSETGLVPTAVHKDSDGGYYCIASNDAGSARCEQEMEYVDL 240
 DB 181 PTDSRANPRFRNSSPHLNSSETGLVPTAVHKDSDGGYYCIASNDAGSARCEQEMEYVDL 240
 QY 241 NIGGIIGGVVLVLAVALITLIGICCAAYRRGYFINNKQDGSYKNPKGPDGVNVRTDDEG 300
 DB 241 NIGGIIGGVVLVLAVALITLIGICCAAYRRGYFINNKQDGSYKNPKGPDGVNVRTDDEG 300
 QY 301 DFRHKSSPVI 310
 DB 301 DFRHKSSPVI 310
 RESULT 8
 AAB80383
 ID AAB80383 standard; protein; 310 AA.
 XX AAB80383;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Secreted protein encoded by gene #13.
 XX
 KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
 KW cerebrovascular; infection; food.
 XX
 OS Homo sapiens.
 XX
 PN WO200107459-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 20-JUL-2000; 2000WO-US019735.
 XX
 PR 23-JUL-1999; 99US-0145220P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
 PI Shi Y, Lafleur DW, Olsen HS, Birse CS, Komatsoulis GA;
 XX WPI; 2001-123261/13.
 DR
 XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
 PT preventing and treating e.g. autoimmune, hyperproliferative,
 PT cardiovascular, and ocular diseases or disorders and microorganism
 PT infections.
 XX
 PS Claim 11; Page 538-539; 601pp; English.
 XX
 CC The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. Also used in food
 CC preparations
 XX
 SQ Sequence 310 AA;


```
Query Match      100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPPLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQSFVELSCIITDSQT 60
DB 1 MALRRPPLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQSFVELSCIITDSQT 60

QY 61 SDPRIEMKKIQDEQTYTTFVFNKIQGDLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDEQTYTTFVFNKIQGDLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120

QY 121 NDRKEIDBIVIELTVQVKPVPVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDBIVIELTVQVKPVPVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240

QY 241 NIGGIIGGVVLAVLALITIGICCAVRRGYFINNKQDGSYKNGPKDGVNYIRTDSEG 300
DB 241 NIGGIIGGVVLAVLALITIGICCAVRRGYFINNKQDGSYKNGPKDGVNYIRTDSEG 300

QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310

RESULT 9
AAB80408
ID AAB80408 standard; protein; 310 AA.
AC AAB80408;
XX
XX
XX 24-APR-2001 (first entry)
XX
XX Secreted protein encoded by gene #38.
XX Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
XX cerebrovascular; infection; food.
XX Homo sapiens.
XX WO200107459-A1.
XX
XX 20-JUL-2000; 2000WO-US019735.
XX
XX 23-JUL-1999; 99US-0145220P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
XX Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX WPI; 2001-123261/13.
XX
XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
XX preventing and treating e.g. autoimmune, hyperproliferative,
XX cardiovascular, and ocular diseases or disorders and microorganism
XX infections.
XX Claim 11; Page 557-558; 601pp; English.
XX
XX The present invention relates to 29 human secreted proteins. The
XX invention is used to prevent autoimmune diseases e.g. rheumatoid
XX arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
XX liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
XX disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
XX e.g. Alzheimer's disease, infections caused by bacteria, viruses and
XX fungi and ocular disorders e.g. corneal infection. Also used in food
```

```
CC preparations
SQ Sequence 310 AA;

Query Match      100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPPLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQSFVELSCIITDSQT 60
DB 1 MALRRPPLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQSFVELSCIITDSQT 60

QY 61 SDPRIEMKKIQDEQTYTTFVFNKIQGDLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDEQTYTTFVFNKIQGDLAGRAEILGKTSLKIMNVTTRDSALYRCEVVAR 120

QY 121 NDRKEIDBIVIELTVQVKPVPVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDBIVIELTVQVKPVPVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240

QY 241 NIGGIIGGVVLAVLALITIGICCAVRRGYFINNKQDGSYKNGPKDGVNYIRTDSEG 300
DB 241 NIGGIIGGVVLAVLALITIGICCAVRRGYFINNKQDGSYKNGPKDGVNYIRTDSEG 300

QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310

RESULT 10
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
XX AAB80409;
XX
XX 24-APR-2001 (first entry)
XX
XX Secreted protein encoded by gene #39.
XX Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
XX cerebrovascular; infection; food.
XX Homo sapiens.
XX WO200107459-A1.
XX
XX 01-FEB-2001.
XX
XX 20-JUL-2000; 2000WO-US019735.
XX
XX 23-JUL-1999; 99US-0145220P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
XX Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX WPI; 2001-123261/13.
XX
XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
XX preventing and treating e.g. autoimmune, hyperproliferative,
XX cardiovascular, and ocular diseases or disorders and microorganism
XX infections.
XX Claim 11; Page 559-560; 601pp; English.
XX
XX The present invention relates to 29 human secreted proteins. The
XX invention is used to prevent autoimmune diseases e.g. rheumatoid
XX arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
XX liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
XX disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
XX e.g. Alzheimer's disease, infections caused by bacteria, viruses and
XX fungi and ocular disorders e.g. corneal infection. Also used in food
```

CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischemia, angio genesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. Also used in food
 CC preparations
 XX
 SQ Sequence 310 AA;
 Query Match 100.0%; Score 1637; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNTPVQEFSEVELSCIITDSQT 60
 DB 1 MALRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNTPVQEFSEVELSCIITDSQT 60
 QY 61 SDPRIEMKKIQDEQTTTVPFDNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120
 DB 61 SDPRIEMKKIQDEQTTTVPFDNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120
 QY 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEBHGPHRPHYSWYRNDVPL 180
 DB 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEBHGPHRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFRNSSFLNSETGTLVPTAVHKDDSGQYCIASNDAGSARCSBQEMEVYDL 240
 DB 181 PTDSRANPRFRNSSFLNSETGTLVPTAVHKDDSGQYCIASNDAGSARCSBQEMEVYDL 240
 QY 241 NIGGIIGVVLVAVLALITLGGICAYRRGYFINNKQDGESYKPKGPGVNYIRTDEG 300
 DB 241 NIGGIIGVVLVAVLALITLGGICAYRRGYFINNKQDGESYKPKGPGVNYIRTDEG 300
 QY 301 DFRHKSSPVI 310
 DB 301 DFRHKSSPVI 310
 RESULT 11
 ABG92709
 ID ABG92709 standard; protein; 310 AA.
 XX
 AC ABG92709;
 XX
 DT 18-NOV-2002 (first entry)
 XX
 DE Human secreted protein PRO1868.
 XX
 KW Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
 KW PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
 KW inflammatory disorder; immune related disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
 KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
 KW psoriasis; allergic disease of the lung; graft-versus host disease;
 KW tumour; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2002098506-A1.
 XX
 PD 25-JUL-2002.
 XX
 XX 27-DEC-2001; 2001US-00033301.
 XX
 PR 04-AUG-1998; 98US-0095325P.
 PR 16-DEC-1998; 98US-0112851P.
 PR 16-DEC-1998; 98US-0113145P.
 PR 22-DEC-1998; 98US-0113511P.
 PR 12-JAN-1999; 99US-0115558P.
 PR 12-JAN-1999; 99US-0115565P.
 PR 12-JAN-1999; 99US-0115733P.
 PR 09-FEB-1999; 99US-0119341P.
 PR 10-FEB-1999; 99US-0119537P.
 PR 12-FEB-1999; 99US-0119965P.

PR 02-JUN-1999; 99WO-US012252.
 PR 29-OCT-1999; 99US-0162506P.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 25-MAY-2001; 2001US-00866034.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WI;
 XX
 DR WPI; 2002-690475/74.
 DR N-PSDB; ABS68392.
 XX
 PT Novel secreted and transmembrane polypeptides and polynucleotides useful
 PT for diagnosis and treatment of inflammatory disorders and immune-related
 PT diseases, and identifying modulators.
 XX
 PS Claim 12; Fig 14; 125pp; English.
 CC
 CC The invention relates to an isolated polypeptide having at least 80%
 CC amino acid sequence identity to secreted and transmembrane polypeptides
 CC PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
 CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
 CC cells and antibodies against PRO polypeptides. PRO proteins are useful
 CC for identifying modulators of the polypeptide. PRO1868 useful for the
 CC diagnosis and treatment of inflammatory and immune related diseases
 CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
 CC sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
 CC infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
 CC versus host disease and tumours. PRO nucleic acids are useful for
 CC constructing hybridisation probes for mapping the gene that encodes that
 CC PRO and for the genetic analysis of individuals with genetic disorders,
 CC and for generating transgenic animals which are useful in the development
 CC and screening of therapeutically useful reagents. PRO nucleic acids are
 CC also useful for gene therapy, chromosome identification, and tissue
 CC typing. PRO proteins are useful as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies are useful in
 CC diagnostic assays for PRO, e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO. The present
 CC sequence represents a PRO protein

SQ Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 5; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNTPVQEFSEVELSCIITDSQT 60
 DB 1 MALRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNTPVQEFSEVELSCIITDSQT 60
 QY 61 SDPRIEMKKIQDEQTTTVPFDNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120
 DB 61 SDPRIEMKKIQDEQTTTVPFDNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120
 QY 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEBHGPHRPHYSWYRNDVPL 180
 DB 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEBHGPHRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFRNSSFLNSETGTLVPTAVHKDDSGQYCIASNDAGSARCSBQEMEVYDL 240
 DB 181 PTDSRANPRFRNSSFLNSETGTLVPTAVHKDDSGQYCIASNDAGSARCSBQEMEVYDL 240

QY 241 NIGGIIGVVLVAVLALITIGICAYRRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
 |||||
 Db 241 NIGGIIGVVLVAVLALITIGICAYRRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
 |||||
 QY 301 DFRKSSFVI 310
 |||||
 Db 301 DFRKSSFVI 310
 |||||
 RESULT 12
 ABG91361
 ID ABG91361 standard; protein; 310 AA.
 XX AC
 XX ABG91361;
 XX 29-NOV-2002 (first entry)
 XX DT
 XX Novel human secreted protein #7.
 XX DB
 XX Human; secreted protein; transmembrane protein; gene mapping; transgenic;
 XX KW immunogenic.
 XX KM
 XX OS Homo sapiens.
 XX PN US2002098505-A1.
 XX PD 25-JUL-2002.
 XX PF 28-DEC-2001; 2001US-00033246.
 XX PR 04-AUG-1998; 98US-0095325P.
 PR 16-DEC-1998; 98US-0112851P.
 PR 16-DEC-1998; 98US-0113145P.
 PR 22-DEC-1998; 98US-0113511P.
 PR 22-JAN-1999; 99US-0115558P.
 PR 12-JAN-1999; 99US-0115563P.
 PR 12-JAN-1999; 99US-0115733P.
 PR 09-FEB-1999; 99US-0119341P.
 PR 10-FEB-1999; 99US-0119537P.
 PR 12-FEB-1999; 99US-0119965P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 29-OCT-1999; 99US-0162508P.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99US-0170262P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 25-MAY-2001; 2001US-00866034.
 XX (GETH) GENENTECH INC.
 XX PA
 XX Botstein D, Desnoyers L, Ferrara N, Pong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WI;
 XX WPI; 2002-665999/71.
 DR N-PSDB; ABS67460.
 XX New human secreted and transmembrane (PRO) polypeptides, useful for
 PT treating conditions requiring PRO polypeptides, for screening PRO
 PT antagonists and agonists useful as drug candidates.
 XX Claim 12; Fig 14; 125pp; English.
 PS The invention relates to new human secreted and transmembrane proteins
 CC (PRO) and nucleic acids of the invention. The polypeptides can be

CC administered therapeutically, especially by expressing encoding
 CC polynucleotides, e.g. in therapeutic compositions. They can be used to
 CC screen for PRO polypeptide antagonists and agonists useful to identify
 CC drug candidates. They can also be used to produce antibodies, useful to
 CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
 CC therapeutically (e.g. as antagonists or to target and/or deliver
 CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
 CC produce antisense sequences to inhibit polypeptide production. They can
 CC be used to produce probes and primers useful to detect or isolate
 CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
 CC sequences from other species. They are also useful for gene mapping and
 CC to generate transgenic animals. ABG91355-ABG91363 represent human PRO
 CC amino acid sequences of the invention
 XX SQ

Sequence 310 AA;

Query Match 100.0%; Score 1637; DB 5; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALRRPPLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQSPFSELSCIITDSQT 60
 Db 1 MALRRPPLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQSPFSELSCIITDSQT 60
 |||||
 QY 61 SDPRIEWKIQDEBQTYVFFDNKIQDLAGRAIIGKTSLKINVTTRDSALYRCVVAR 120
 Db 61 SDPRIEWKIQDEBQTYVFFDNKIQDLAGRAIIGKTSLKINVTTRDSALYRCVVAR 120
 |||||
 QY 121 NDRKEIDIVIELTVQVKPVPFCVPRKAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180
 Db 121 NDRKEIDIVIELTVQVKPVPFCVPRKAVPVGMATLHCQSEGHPRPHYSWYRNDVPL 180
 |||||
 QY 181 PTDSRANPRFNSSPHLNSFTGLVFTAVHKDDSQYTCIANDAGSARCEQMEVYDL 240
 Db 181 PTDSRANPRFNSSPHLNSFTGLVFTAVHKDDSQYTCIANDAGSARCEQMEVYDL 240
 |||||
 QY 241 NIGGIIGVVLVAVLALITIGICAYRRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
 Db 241 NIGGIIGVVLVAVLALITIGICAYRRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
 |||||
 QY 301 DFRKSSFVI 310
 |||||
 Db 301 DFRKSSFVI 310
 |||||

RESULT 13

ABB84947
 ID ABB84947 standard; protein; 310 AA.

XX AC ABB84947;

XX 16-MAY-2002 (first entry)

XX Human PRO1868 protein sequence SEQ ID NO:262.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PF 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230798P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Ferrara N, Gerber H, Gerritsen MB, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NP;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR N-PSDB; ABL88202.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 262; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 310 AA;
 Query Match 100.0%; Score 1637; DB 5; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.3e-131;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MALRRPRLRLCARLPDPFLLLPRLGCLIGAVNLKSSNRTPVQBFESVELSCIITDSQT 60
 |||||
 Db 1 MALRRPRLRLCARLPDPFLLLPRLGCLIGAVNLKSSNRTPVQBFESVELSCIITDSQT 60
 Qy 61 SDPRIWKIKIQDRQTTTYPFDNKIQGDLAGRAEILGKTSLKIMWTRDSALYRCVVAR 120
 |||||
 Db 61 SDPRIWKIKIQDRQTTTYPFDNKIQGDLAGRAEILGKTSLKIMWTRDSALYRCVVAR 120
 Qy 121 NDRKEIDIVIELTVQVKPVPVCRVPAVPVGNKMATLHCQESGHPHPRPHYSWYRNDVPL 180
 |||||
 Db 121 NDRKEIDIVIELTVQVKPVPVCRVPAVPVGNKMATLHCQESGHPHPRPHYSWYRNDVPL 180
 Qy 181 PTDSRANPRFRNSPFLNSETGLVFTAVHKDDSQYYCIAASNDAGSARCEQEMEYVDL 240
 |||||
 Db 181 PTDSRANPRFRNSPFLNSETGLVFTAVHKDDSQYYCIAASNDAGSARCEQEMEYVDL 240
 Qy 241 NIGGIIGGLVVLAVLALITIGICCAVRRGYFINNKQGESYKNGKPDGVNVIITDRSG 300
 |||||
 Db 241 NIGGIIGGLVVLAVLALITIGICCAVRRGYFINNKQGESYKNGKPDGVNVIITDRSG 300
 Qy 301 DFRHKSSPVI 310
 |||||
 Db 301 DFRHKSSPVI 310
 RESULT 14
 ABG65297
 ID ABG65297 standard; protein; 310 AA.
 XX AC ABG65297;
 XX DT 27-AUG-2002 (first entry)
 XX DE Human albumin fusion protein #1972.
 XX KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antiinfertility; antiinflammatory; antiulcer;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200177137-A1.
 XX PD 18-OCT-2001.
 XX PF 12-APR-2001; 2001WO-US011988.
 XX PR 12-APR-2000; 2000US-0229358P.
 PR 25-APR-2000; 2000US-0199384P.
 PR 21-DEC-2000; 2000US-0256931P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Haseltine WA;
 WPI; 2002-010886/01.
 DR New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein.
 XX
 PS Claim 1; Page 1895; 2102pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA), also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or disorder
 CC that may be modulated by therapeutic protein X. The albumin extends the
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo
 CC activity. The protein is useful for treating and diagnosing disorders
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's

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CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ Sequence 310 AA;

Query Match      100.0%; Score 1637; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
QY 61 SDPRIEMKKIQDBQTTVFFDNKIQDLAGRAEILGKTSLKINWVTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDBQTTVFFDNKIQDLAGRAEILGKTSLKINWVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
QY 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDSSGQYICIASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDSSGQYICIASNDAGSARCEQEMEVYDL 240
QY 241 NIGGIIGGVLVLAVALALITLIGICCAVRRGYFINNKDGESYKPKGPDGVNVRTDEEG 300
DB 241 NIGGIIGGVLVLAVALALITLIGICCAVRRGYFINNKDGESYKPKGPDGVNVRTDEEG 300
QY 301 DFRHKSFPVI 310
DB 301 DFRHKSFPVI 310

RESULT 15
ABG65296
ID ABG65296 standard; protein; 310 AA.
XX
AC ABG65296;
XX
XX 27-AUG-2002 (first entry)
DE Human albumin fusion protein #1971.
XX
KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytostatic; anti-infectivity; anti-inflammatory; anti-ulcer;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177137-A1.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011988.
XX
PR 12-APR-2000; 2000US-0229358P.
PR 25-APR-2000; 2000US-0199384P.
XX 21-DEC-2000; 2000US-0256931P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Haseltine WA;

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XX WPI; 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1893-1894; 2102pp; English.
XX
CC The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA, also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or disorder
CC that may be modulated by therapeutic protein X. The albumin extends the
CC shelf-life of protein X, and may increase its biological in vitro/in vivo
CC activity. The protein is useful for treating and diagnosing disorders
CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ Sequence 310 AA;

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```

Query Match      100.0%; Score 1637; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.3e-131;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
QY 61 SDPRIEMKKIQDBQTTVFFDNKIQDLAGRAEILGKTSLKINWVTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDBQTTVFFDNKIQDLAGRAEILGKTSLKINWVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
QY 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDSSGQYICIASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDSSGQYICIASNDAGSARCEQEMEVYDL 240
QY 241 NIGGIIGGVLVLAVALALITLIGICCAVRRGYFINNKDGESYKPKGPDGVNVRTDEEG 300
DB 241 NIGGIIGGVLVLAVALALITLIGICCAVRRGYFINNKDGESYKPKGPDGVNVRTDEEG 300
QY 301 DFRHKSFPVI 310
DB 301 DFRHKSFPVI 310

```

Search completed: June 15, 2004, 11:03:07
Job time : 52.5 sec

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: June 15, 2004, 11:03:45 ; Search time 51 Seconds
(without alignments)
1717.446 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYLPHFL.....VNYRTSEGDPRKHSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	310	100.0	310	3	AAB27278	Aab27278 Murine co
2	310	100.0	310	3	AAB27272	Aab27272 Human con
3	24	7.7	285	3	AAB39254	Aab39254 Human sec
4	24	7.7	291	4	ABG04645	Abg04645 Novel hum
5	24	7.7	310	3	AAY96294	Aay96294 Human IGF
6	24	7.7	310	3	AAY96735	Aay96735 PRO1868
7	24	7.7	310	3	AB333457	Ab333457 Human PRO
8	24	7.7	310	3	AAB27276	Aab27276 Human con
9	24	7.7	310	4	AAB80272	Aab80272 Human PRO
10	24	7.7	310	4	AAM93905	Aam93905 Human pol
11	24	7.7	310	4	AAM93323	Aam93323 Human pol
12	24	7.7	310	4	AAM12440	Aam12440 Human PRO
13	24	7.7	310	4	AAB80383	Aab80383 Secreted
14	24	7.7	310	4	AAB80408	Aab80408 Secreted
15	24	7.7	310	4	AAB80409	Aab80409 Secreted
16	24	7.7	310	5	ABG92709	Abg92709 Human sec
17	24	7.7	310	5	ABG91361	Abg91361 Novel hum
18	24	7.7	310	5	AB884947	Ab884947 Human PRO
19	24	7.7	310	5	ABG65297	Abg65297 Human alb
20	24	7.7	310	5	ABG65296	Abg65296 Human alb
21	24	7.7	310	5	ABG65298	Abg65298 Human alb
22	24	7.7	310	5	ABG31401	Abg31401 Human PRO
23	24	7.7	310	5	AB895553	Ab895553 Human ang
24	24	7.7	310	6	ABU71650	Abu71650 Human PRO
25	24	7.7	310	6	ABU72377	Abu72377 Novel hum

26	24	7.7	310	6	ABU80867	Abu80867 Human sec
27	24	7.7	310	6	ABO17884	Abol7884 Novel hum
28	24	7.7	310	6	ABU71505	Abu71505 Human PRO
29	24	7.7	310	6	ADA57610	Ada57610 Human sec
30	24	7.7	310	6	ADA57611	Ada57611 Human sec
31	24	7.7	310	6	ADA57309	Ada57309 Human sec
32	24	7.7	310	6	ABP71277	Abp71277 Human jun
33	24	7.7	310	6	ABP71277	Abp71277 Human jun
34	24	7.7	310	6	ABU81138	Abu81138 Human PRO
35	24	7.7	310	6	ABU71951	Abu71951 Human sec
36	24	7.7	310	6	ABO01834	Abou01834 Novel hum
37	24	7.7	310	6	ABU66838	Abu66838 Human PRO
38	24	7.7	310	6	ABU54407	Abu54407 Human sec
39	24	7.7	310	6	ABO47422	Abu47422 Human sec
40	24	7.7	310	6	ABG73314	Abg73314 Human PRO
41	24	7.7	310	6	ABU59919	Abu59919 Novel sec
42	24	7.7	310	6	ABO25109	Abos25109 Human sec
43	24	7.7	310	6	ABU64559	Abu64559 Human sec
44	24	7.7	310	6	ABU67405	Abu67405 Human sec
45	24	7.7	310	6	ABO14925	Abol14925 Human sec
					ABU60813	Human sec

ALIGNMENTS

RESULT 1
AAB27278
ID AAB27278 standard; protein; 310 AA.
XX
AC AAB27278;
XX
DT 23-FEB-2001 (first entry)
XX
DB Murine confluency regulated adhesion molecule 1.
XX
KW Immunoglobulin superfamily; Ig sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; mouse;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Mus sp.
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-BP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMP DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI: 2000-587436/55.
XX
PS N-PSDB; AAA97189.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or CRAM-2) polypeptide, useful for treatment of tumors, inflammation reactions and modulating vascular permeability.
XX
PS Example; Fig 8; 59pp; English.
XX
CC The present sequence is the murine confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfamily (ig sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, and modulating cell-cell interactions and angiogenesis, and in the modulation of wound healing
XX
SQ Sequence 310 AA;
Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.4e-288;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLARLPHFFLLPRGCMIBAVNLKSSNRNPVHVEFESVLSLCIITHSQT 60
Db 1 MALSRRLRLRLYLARLPHFFLLPRGCMIBAVNLKSSNRNPVHVEFESVLSLCIITHSQT 60
Qy 61 SDPRIWKIKIQDQTTVVYFDNKKIQGLAGRTDVFGKTSLRIMNVTRSDSAIYRCEVVAL 120
Db 61 SDPRIWKIKIQDQTTVVYFDNKKIQGLAGRTDVFGKTSLRIMNVTRSDSAIYRCEVVAL 120
Qy 121 NDRKEVDEITIELIVQKPTVPCRIIPAAVPVGKTATLQCESGEGYPRPHYSWYRNDVPL 180
Db 121 NDRKEVDEITIELIVQKPTVPCRIIPAAVPVGKTATLQCESGEGYPRPHYSWYRNDVPL 180
Qy 181 PTDSTRANPRFQNSFHVNSGTGLVFNVAHKDSDGQYYCIASNDAGAARCEGQDMEVYDL 240
Db 181 PTDSTRANPRFQNSFHVNSGTGLVFNVAHKDSDGQYYCIASNDAGAARCEGQDMEVYDL 240
Qy 241 NIAGIIGGVLLVLLVLAIVTMGICCAVRCGCFISSKQDGSYKSPGKHGDNVYIRTSEEG 300
Db 241 NIAGIIGGVLLVLLVLAIVTMGICCAVRCGCFISSKQDGSYKSPGKHGDNVYIRTSEEG 300
Qy 301 DFRKSSFVI 310
Db 301 DFRKSSFVI 310

RESULT 2
AAB27272
ID AAB27272 standard; protein; 310 AA.
AC AAB27272;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human confluency regulated adhesion molecule 1 #1.
XX
KW Immunoglobulin superfamily; Ig S; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; human;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Homo sapiens.
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMP DICTAGENE SA.
XX
PI Imhof BA, Aurtrand-Lions M;
XX
DR WPI; 2000-587436/55.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Claim 1; Fig 3; 59pp; English.
XX
CC The present sequence is the human confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig S). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
SQ Sequence 310 AA;
Query Match 100.0%; Score 310; DB 3; Length 310;

Best Local Similarity 100.0%; Pred. No. 2.4e-288;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLARLPHFFLLPRGCMIBAVNLKSSNRNPVHVEFESVLSLCIITHSQT 60
Db 1 MALSRRLRLRLYLARLPHFFLLPRGCMIBAVNLKSSNRNPVHVEFESVLSLCIITHSQT 60
Qy 61 SDPRIWKIKIQDQTTVVYFDNKKIQGLAGRTDVFGKTSLRIMNVTRSDSAIYRCEVVAL 120
Db 61 SDPRIWKIKIQDQTTVVYFDNKKIQGLAGRTDVFGKTSLRIMNVTRSDSAIYRCEVVAL 120
Qy 121 NDRKEVDEITIELIVQKPTVPCRIIPAAVPVGKTATLQCESGEGYPRPHYSWYRNDVPL 180
Db 121 NDRKEVDEITIELIVQKPTVPCRIIPAAVPVGKTATLQCESGEGYPRPHYSWYRNDVPL 180
Qy 181 PTDSTRANPRFQNSFHVNSGTGLVFNVAHKDSDGQYYCIASNDAGAARCEGQDMEVYDL 240
Db 181 PTDSTRANPRFQNSFHVNSGTGLVFNVAHKDSDGQYYCIASNDAGAARCEGQDMEVYDL 240
Qy 241 NIAGIIGGVLLVLLVLAIVTMGICCAVRCGCFISSKQDGSYKSPGKHGDNVYIRTSEEG 300
Db 241 NIAGIIGGVLLVLLVLAIVTMGICCAVRCGCFISSKQDGSYKSPGKHGDNVYIRTSEEG 300
Qy 301 DFRKSSFVI 310
Db 301 DFRKSSFVI 310

RESULT 3
AAB39254
ID AAB39254 standard; protein; 285 AA.
XX
AC AAB39254;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective;
KW neotropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
KW ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis;
KW hyperproliferative disorder; cardiovascular disorder; infection;
KW cerebrovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; chemotaxis.
XX
OS Homo sapiens.
XX
PN WO200056754-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US006792.
XX
PR 19-MAR-1999; 99US-0125362P.
PR 10-DEC-1999; 99US-0169980P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen GA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-579483/54.
DR N-PSDB; AAC74237.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 32; 434pp; English.
XX
CC The polynucleotide sequences given in AAC74223-C74279 encode the human
CC secreted proteins represented in AAB39179-B39226. Sequences AAB39227-
CC B39308 are alternative proteins encoded by the genes, and also protein
CC sequences with which they share homology. The proteins have activities

CC based on the tissues and cells in which they are expressed. Examples of
 CC activities include: immunosuppressive; antiarthritic; antirheumatic;
 CC antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective;
 CC neoplastic; neuroprotective; antibacterial; virucide; fungicide; and
 CC ophthalmologic. The human secreted proteins, polynucleotides,
 CC antagonists and agonists of the invention may be useful in the treatment,
 CC prevention, and/or diagnosis of various disease, disorders and conditions
 CC such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to regenerate tissues,
 CC maintain organs before transplantation, in chemotaxis and as a food
 CC additive or preservative e.g. to increase storage capabilities. Sequences
 CC AAC74214-C74222 and AAB39178 are used during the isolation and
 CC characterisation of the genes of the invention
 CC
 XX
 SQ Sequence 285 AA;

Query Match 7.7%; Score 24; DB 3; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
 |||||
 DB 142 PRPHYSWYRNDVPLPTDSRANPRF 165

RESULT 4
 ABG04645
 ID ABG04645 standard; protein; 291 AA.

XX
 AC ABG04645;
 XX
 DT 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #4636.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSB-) HYSEQ INC.

XX Dmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS68832.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 35004; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of DNA and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 291 AA;

Query Match 7.7%; Score 24; DB 4; Length 291;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
 |||||
 DB 214 PRPHYSWYRNDVPLPTDSRANPRF 237

RESULT 5
 AAY96294
 ID AAY96294 standard; protein; 310 AA.

XX
 AC AAY96294;

XX 16-AUG-2000 (first entry)

XX Human IGFAM-6 immunoglobulin.

XX Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..30

FT Protein /label= signal_peptide

FT Domain 31..310

FT Domain 46..117

FT Domain 153..221

FT Domain /label= Ig_domain

FT Domain 238..260

FT Domain /label= transmembrane_domain

XX WO200029583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

XX 19-NOV-1998; 98US-00195853.

XX 22-DEC-1998; 98US-0113635P.

XX 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H. Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

XX Lu DAM, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27386.

PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
 PT protein is useful for preventing and treating disorders associated with
 PT altered levels of the protein such as cancer, immune system disorders.
 XX
 PS
 XX Claim 1; Page 82-83; 105pp; English.
 XX
 XX The present sequence is the human immunoglobulin superfamily protein
 CC IGFAM-6. Its gene was isolated from a cDNA library of leg tissue. It is
 CC expressed in reproductive, nervous and cardiovascular tissue, where
 CC cancer and inflammation are common. The gene, protein, its antibodies,
 CC agonists and antagonists are suitable for diagnosing and treating many
 CC diseases, including cancer, immune system disorders (such as
 CC inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,
 CC atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,
 CC emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,
 CC rheumatoid arthritis, scleroderma, systemic lupus erythematosus and
 CC ulcerative colitis), complications of cancer, haemodialysis and
 CC extracorporeal circulation, trauma and haematopoietic cancer (such as
 CC leukaemia) and infections caused by bacteria, viruses, fungi or parasites
 XX
 XX Sequence 310 AA;

Query Match 7.7%; Score 24; DB 3; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVPLPTDSRANPRF 190
 |||||
 Db 167 PRPHYSWRNDVPLPTDSRANPRF 190

RESULT 6
 ID AAY96735 standard; protein; 310 AA.

AC AAY96735;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 XX PRO1868, an A33 antigen homologue.
 XX
 XX PRO1868; A33 antigen; secreted protein; transmembrane protein;
 KW anti-inflammatory; cytostatic; recombinant production; gene therapy.
 KW
 XX Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..30
 FT /label= Signal_peptide
 FT Modified-site 26..31
 FT /note= "N-myristoylation site"
 FT Modified-site 69..77
 FT /note= "Tyrosine kinase phosphorylation site"
 FT Modified-site 104..107
 FT /note= "N-glycosylation site"
 FT Modified-site 106..109
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 107..110
 FT /note= "CAMP- and cGMP-dependent protein kinase
 FT phosphorylation site"
 FT Modified-site 192..195
 FT /note= "N-glycosylation site"
 FT Modified-site 215..220
 FT /note= "N-myristoylation site"
 FT Modified-site 226..231
 FT /note= "N-myristoylation site"
 FT Domain 243..263
 FT /label= Transmembrane_domain
 FT Modified-site 243..248
 FT /note= "N-myristoylation site"
 FT Modified-site 244..249
 FT /note= "N-myristoylation site"
 FT Modified-site 262..267

FT /note= "N-myristoylation site"
 FT Modified-site 296..299
 FT /note= "Casein kinase II phosphorylation site"

XX WO200036102-A2.

XX 22-JUN-2000.

XX 01-DEC-1999; 99WO-US028634.

XX 16-DEC-1998; 98US-0112851P.

XX 16-DEC-1998; 98US-0113145P.

XX 22-DEC-1998; 98US-0113511P.

XX 12-JAN-1999; 99US-0115586P.

XX 12-JAN-1999; 99US-0115565P.

XX 09-FEB-1999; 99US-0115733P.

XX 10-FEB-1999; 99US-0119341P.

XX 12-FEB-1999; 99US-0119537P.

XX 12-FEB-1999; 99US-0119665P.

XX 02-JUN-1999; 99WO-US012252.

XX (GETH) GENENTECH INC.

XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;

XX Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;

XX Wood WI;

XX WPI; 2000-431586/37.

XX N-PSDB; AAA51265.

XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a

XX transmembrane polypeptide.

XX Claim 1; Fig 14; 154pp; English.

XX This is PRO1868, a putative homologue of A33 antigen, a known colorectal

XX cancer-associated marker. The invention concerns novel secreted and

XX transmembrane proteins, designated PRO polypeptides. The cDNA and gene

XX sequences are useful in the recombinant production of PRO polypeptides,

XX as a hybridization probe to screen libraries to isolate cDNAs with

XX sequence identity to PRO polypeptides or to map the gene encoding the PRO

XX polypeptides and analyzing genetic disorders. The cDNA/gene can also be

XX used to produce transgenic animals useful for the development and

XX screening of therapeutically useful reagents. They can also be used in

XX gene therapy, e.g. to replace a defective gene

XX Sequence 310 AA;

XX Query Match 7.7%; Score 24; DB 3; Length 310;

XX Best Local Similarity 100.0%; Pred. No. 2.5e-14;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVPLPTDSRANPRF 190
 |||||
 Db 167 PRPHYSWRNDVPLPTDSRANPRF 190

RESULT 7

AAAB33457

ID AAB33457 standard; protein; 310 AA.

XX AAB33457;

XX 29-JAN-2001 (first entry)

XX Human PRO1868 protein UNQ859 SEQ ID NO:193.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatologic; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
 KW antianthematic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;

KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
XX OS
XX WO200053758-A2.
XX PN
XX PD 14-SEP-2000.
XX XX
XX PF 02-MAR-2000; 2000WO-US005841.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1999; 99US-0123618P.
XX PR 12-MAR-1999; 99US-0123957P.
XX PR 23-MAR-1999; 99US-0123775P.
XX PR 12-APR-1999; 99US-0128849P.
XX PR 20-APR-1999; 99WO-US008615.
XX PR 28-APR-1999; 99US-0131445P.
XX PR 04-MAY-1989; 99US-0132371P.
XX PR 14-MAY-1999; 99US-0134287P.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 05-OCT-1999; 99WO-US023089.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 29-NOV-1999; 99WO-US028214.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 30-NOV-1999; 99WO-US028409.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US000356.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.
XX PR 22-FEB-2000; 2000WO-US004414.
XX (GETH) GENENTECH INC.
XX PA
XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
XX PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
XX PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M,
XX N-PSDB; AAC58622.
XX DR WPI; 2000-572271/53.
XX N-PSDB; AAC58622.
XX XX
XX PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX XX
XX PS Claim 33; Fig 88; 309pp; English.
XX PS
XX CC The present invention describes sixty four human PRO proteins which can

CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
XX SQ Sequence 310 AA;
XX
XX Query Match 7.7%; Score 24; DB 3; Length 310;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-14;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 167 PRPHYSWYRNDVPLPTDSRANPRP 190
XX DB 167 PRPHYSWYRNDVPLPTDSRANPRP 190
XX
XX RESULT 8
XX AAB27276
XX ID AAB27276 standard; protein; 310 AA.
XX XX
XX AC AAB27276;
XX XX
XX DT 23-FEB-2001 (first entry)
XX XX
XX DE Human confluency regulated adhesion molecule 1 #2.
XX XX
XX KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
XX KW inflammation; cancer; wound; angiogenesis; human;
XX KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200053749-A2.
XX XX
XX PD 14-SEP-2000.
XX XX
XX PF 13-MAR-2000; 2000WO-EP002219.
XX XX
XX PR 11-MAR-1999; 99EP-00200746.
XX XX
XX PA (RMFD-) RMF DICTAGENE SA.
XX XX
XX PI Imhof BA, Aurand-Lions M;
XX XX
XX DR WPI; 2000-587436/55.
XX N-PSDB; AAA95306.
XX XX
XX PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
XX PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
XX PT reactions and modulating vascular permeability.
XX PS
XX PS Claim 2; Fig 6; 59pp; English.
XX XX
XX CC The present sequence is the human confluency regulated adhesion molecule
XX CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
XX CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
XX CC and coding sequence can be used in the treatment of cancer, inflammation,
XX CC to modulate cell-cell interactions and angiogenesis, and in the
XX CC modulation of wound healing

XX SQ Sequence 310 AA;
 Query Match 7.7%; Score 24; DB 3; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
 DB 167 PRPHYSWYRNDVPLPTDSRANPRF 190
 RESULT 9
 AAB80272
 ID AAB80272 standard; protein; 310 AA.
 AC AAB80272;
 DT 24-APR-2001 (first entry)
 DE Human PRO1868 protein.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian neurotropic; neuroprotective; vulnerrary; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000WO-US004414.
 XX
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 03-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N,
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ,
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2001-081051/09.
 DR N-PSDB; AAF72433.
 XX
 XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 PT disease).
 XX
 XX Claim 1; Fig 124; 393pp; English.
 PS
 XX The present sequence is one of sixty one novel secreted and transmembrane
 CC

CC PRO polypeptides. The PRO polypeptides are useful for treating skin
 CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
 CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosum. The PRO nucleic acids have applications in molecular and
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping
 XX
 SQ Sequence 310 AA;
 Query Match 7.7%; Score 24; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
 DB 167 PRPHYSWYRNDVPLPTDSRANPRF 190
 RESULT 10
 AAM93905
 ID AAM93905 standard; protein; 310 AA.
 XX
 AC AAM93905;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide, SEQ ID NO: 4051.
 XX
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 PN EP1130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR N-PSDB; AAK94867.
 XX
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 XX
 XX Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
 PS
 XX The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO

SQ Sequence 310 AA;
 Query Match 7.7%; Score 24; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHYSWYRNDVPLPTDSRANRP 190
 Db 167 PRPHYSWYRNDVPLPTDSRANRP 190

RESULT 11
 AAM93323
 ID AAM93323 standard; protein; 310 AA.
 XX AC AAM93323;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide, SEQ ID NO: 2845.
 XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX OS Homo sapiens.
 XX EN EP1130094-A2.
 XX PD 05-SEP-2001.
 XX PF 07-JUL-2000; 2000EP-00114089.
 XX PR 08-JUL-1999; 99JP-00194486.
 XX PR 11-JAN-2000; 2000JP-00118774.
 XX PR 02-MAY-2000; 2000JP-00183765.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX DR WPI; 2001-524255/58.
 XX DR N-PSDB; AAK94243.
 XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO

SQ Sequence 310 AA;
 Query Match 7.7%; Score 24; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 PRPHYSWYRNDVPLPTDSRANRP 190
 Db 167 PRPHYSWYRNDVPLPTDSRANRP 190

RESULT 12
 AAM93323
 ID AAM93323 standard; protein; 310 AA.
 XX AC AAM93323;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide, SEQ ID NO: 2845.
 XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX OS Homo sapiens.
 XX EN EP1130094-A2.
 XX PD 05-SEP-2001.
 XX PF 07-JUL-2000; 2000EP-00114089.
 XX PR 08-JUL-1999; 99JP-00194486.
 XX PR 11-JAN-2000; 2000JP-00118774.
 XX PR 02-MAY-2000; 2000JP-00183765.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX DR WPI; 2001-524255/58.
 XX DR N-PSDB; AAK94243.
 XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO

AAU12440
 ID AAU12440 standard; protein; 310 AA.
 XX AC AAU12440;
 XX DT 24-OCT-2001 (first entry)
 XX DE Human PRO1868 polypeptide sequence.
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200140466-A2.
 XX PD 07-JUN-2001.
 XX PF 01-DEC-2000; 2000WO-US032678.
 XX PR 01-DEC-1999; 99WO-US028301.
 XX PR 01-DEC-1999; 99WO-US028634.
 XX PR 02-DEC-1999; 99WO-US028551.
 XX PR 02-DEC-1999; 99WO-US028564.
 XX PR 02-DEC-1999; 99WO-US028565.
 XX PR 09-DEC-1999; 99US-0170262P.
 XX PR 16-DEC-1999; 99WO-US030095.
 XX PR 20-DEC-1999; 99WO-US030911.
 XX PR 20-DEC-1999; 99WO-US030999.
 XX PR 30-DEC-1999; 99WO-US031243.
 XX PR 30-DEC-1999; 99WO-US031274.
 XX PR 05-JAN-2000; 2000WO-US000219.
 XX PR 06-JAN-2000; 2000WO-US000277.
 XX PR 06-JAN-2000; 2000WO-US000376.
 XX PR 11-FEB-2000; 2000WO-US003565.
 XX PR 18-FEB-2000; 2000WO-US004341.
 XX PR 18-FEB-2000; 2000WO-US004342.
 XX PR 22-FEB-2000; 2000WO-US004414.
 XX PR 24-FEB-2000; 2000WO-US004914.
 XX PR 24-FEB-2000; 2000WO-US005004.
 XX PR 01-MAR-2000; 2000WO-US005601.
 XX PR 02-MAR-2000; 2000WO-US005841.
 XX PR 03-MAR-2000; 2000US-0187202P.
 XX PR 10-MAR-2000; 2000WO-US006319.
 XX PR 15-MAR-2000; 2000WO-US006884.
 XX PR 20-MAR-2000; 2000WO-US007377.
 XX PR 21-MAR-2000; 2000WO-US007532.
 XX PR 30-MAR-2000; 2000WO-US008439.
 XX PR 17-MAY-2000; 2000WO-US013705.
 XX PR 22-MAY-2000; 2000WO-US014042.
 XX PR 30-MAY-2000; 2000WO-US014941.
 XX PR 02-JUN-2000; 2000WO-US015264.
 XX PR 05-JUN-2000; 2000US-0209832P.
 XX PR 28-JUL-2000; 2000WO-US020710.
 XX PR 11-AUG-2000; 2000WO-US022031.
 XX PR 23-AUG-2000; 2000WO-US023522.
 XX PR 24-AUG-2000; 2000WO-US023328.
 XX PR 08-NOV-2000; 2000WO-US030952.
 XX PR 10-NOV-2000; 2000WO-US030873.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-408281/43.
 XX DR N-PSDB; AAS21512.
 XX PT Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO

PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX Claim 12; Fig 538; 813pp; English.
 PS
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, and to detect the presence of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 XX Sequence 310 AA;
 SQ
 Query Match 7.7%; Score 24; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 PRPHYSWYRNDVPLTDSRANPRF 190
 DB 167 PRPHYSWYRNDVPLTDSRANPRF 190
 |||||
 RESULT 13
 AAB80383
 ID AAB80383 standard; protein; 310 AA.
 AC AAB80383;
 XX
 XX 24-APR-2001 (first entry)
 DT
 XX Secreted protein encoded by gene #13.
 DE
 XX Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
 KW cerebrovascular; infection; food.
 XX
 XX Homo sapiens.
 OS
 XX W0200107459-A1.
 XX
 XX 01-FEB-2001.
 PD
 XX 20-JUL-2000; 2000WO-US019735.
 PP
 XX 23-JUL-1999; 99US-0145220P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
 PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
 XX WPI; 2001-123261/13.
 DR
 XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
 PT preventing and treating e.g. autoimmune, hyperproliferative,
 PT cardiovascular, and ocular diseases or disorders and microorganism
 PT infections.
 XX
 XX Claim 11; Page 538-539; 601pp; English.
 PS

XX The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. Also used in food
 CC preparations
 XX
 XX Sequence 310 AA;
 SQ
 Query Match 7.7%; Score 24; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 PRPHYSWYRNDVPLTDSRANPRF 190
 DB 167 PRPHYSWYRNDVPLTDSRANPRF 190
 |||||
 RESULT 14
 AAB80408
 ID AAB80408 standard; protein; 310 AA.
 XX
 XX AAB80408;
 AC
 XX
 XX 24-APR-2001 (first entry)
 DT
 XX Secreted protein encoded by gene #38.
 DE
 XX Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
 KW cerebrovascular; infection; food.
 XX
 XX Homo sapiens.
 OS
 XX W0200107459-A1.
 XX
 XX 01-FEB-2001.
 PD
 XX 20-JUL-2000; 2000WO-US019735.
 PP
 XX 23-JUL-1999; 99US-0145220P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
 PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
 XX WPI; 2001-123261/13.
 DR
 XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
 PT preventing and treating e.g. autoimmune, hyperproliferative,
 PT cardiovascular, and ocular diseases or disorders and microorganism
 PT infections.
 XX
 XX Claim 11; Page 557-558; 601pp; English.
 PS
 XX The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. Also used in food
 CC preparations
 XX
 XX Sequence 310 AA;
 SQ
 Query Match 7.7%; Score 24; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
DB 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 15

AAB80409
ID AAB80409 standard; protein; 310 AA.

XX AC AAB80409;

XX DT 24-APR-2001 (first entry)

XX DE Secreted protein encoded by gene #39.

XX KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;

XX KW cerebrovascular; infection; food.

XX OS Homo sapiens.

XX PN WO200107459-A1.

XX PD 01-FEB-2001.

XX PF 20-JUL-2000; 2000WO-US019735.

XX PR 23-JUL-1999; 99US-0145220P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;

XX PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;

XX DR WPI; 2001-123261/13.

XX PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.

XX PS Claim 11; Page 559-560; 601pp; English.

XX CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations

XX SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. NO. 2.5e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190

DB 167 PRPHYSWYRNDVPLPTDSRANPRF 190

Search completed: June 15, 2004, 11:09:56
Job time : 51 secs

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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:08:05 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531c-13

Perfect score: 310

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Gapop 60.0 , Capext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	24	7.7	310	4	US-09-505-125A-423
3	24	7.7	310	4	US-09-902-775A-423
4	8	2.6	48	1	US-08-485-455B-65
5	8	2.6	48	2	US-08-482-130C-65
6	8	2.6	48	2	US-08-484-211C-65
7	8	2.6	48	3	US-08-906-769-65
8	8	2.6	48	3	US-08-906-616-65
9	8	2.6	48	3	US-08-917-795-65
10	8	2.6	48	3	US-08-485-443B-65
11	8	2.6	48	3	US-08-639-075A-65
12	8	2.6	48	3	US-09-012-431-65
13	8	2.6	48	3	US-09-012-692-65
14	8	2.6	48	3	US-08-906-613-65
15	8	2.6	48	5	PCT-US95-1442A-65
16	8	2.6	208	4	US-09-134-001C-3209
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18	8	2.6	246	3	US-08-906-616-127
19	8	2.6	246	3	US-08-639-075A-127
20	8	2.6	246	3	US-09-012-431-127
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22	8	2.6	246	3	US-08-906-613-127
23	8	2.6	421	4	US-09-252-991A-30177
24	8	2.6	530	4	US-09-252-991A-28311
25	7	2.3	24	4	US-10-053-485-34
26	7	2.3	107	4	US-08-999-689A-25
27	7	2.3	147	4	US-09-252-991A-26005

Sequence 2, Appli
Sequence 2, Appli
Sequence 30173, A
Sequence 20017, A
Sequence 1, Appli
Sequence 29543, A
Sequence 28605, A
Sequence 32717, A
Sequence 25451, A
Sequence 23711, A
Sequence 20555, A
Sequence 5241, Ap
Sequence 3948, Ap
Sequence 7127, Ap
Sequence 21539, A
Sequence 18576, A
Sequence 19154, A

28 7 2.3 170 3 US-09-189-035-2
29 7 2.3 170 3 US-09-382-086-2
30 7 2.3 227 4 US-09-252-991A-30173
31 7 2.3 230 4 US-09-252-991A-20017
32 7 2.3 249 3 US-09-154-802-1
33 7 2.3 249 3 US-09-373-029-1
34 7 2.3 293 4 US-09-252-991A-29543
35 7 2.3 303 4 US-09-252-991A-28605
36 7 2.3 372 4 US-09-252-991A-32717
37 7 2.3 410 4 US-09-252-991A-25451
38 7 2.3 411 4 US-09-252-991A-23711
39 7 2.3 450 4 US-09-252-991A-20555
40 7 2.3 489 4 US-09-134-001C-5241
41 7 2.3 503 4 US-09-134-001C-3948
42 7 2.3 526 4 US-09-107-532A-7127
43 7 2.3 539 4 US-09-252-991A-21539
44 7 2.3 547 4 US-09-252-991A-18576
45 7 2.3 659 4 US-09-252-991A-19154

ALIGNMENTS

RESULT 1

US-09-907-794A-423
Sequence 423, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. NO. 1.9e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVLPFTDSRANPRF 190
Db 167 PRPHYSWRNDVLPFTDSRANPRF 190

RESULT 2

US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905.125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. NO. 1.9e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVLPFTDSRANPRF 190
Db 167 PRPHYSWRNDVLPFTDSRANPRF 190

RESULT 3

US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 668451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-775A-423

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 4
US-08-485-455D-65
Sequence 65, Application US/08485455D
Patent No. 5712143
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-775A-423

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 4
US-08-485-455D-65
Sequence 65, Application US/08485455D
Patent No. 5712143
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,455D
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-455D-65

Query Match 2.6%; Score 8; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
Db 1 VLIVLAVI 8

RESULT 5
US-08-482-130C-65
Sequence 65, Application US/08482130C
Patent No. 5982257
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,130C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-1
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-130C-65

Query Match 2.6%; Score 8; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
| | | | |
Db 1 VLIVLAVI 8

RESULT 6

US-08-484-211C-65
; Sequence 65, Application US/08484211C
; Patent No. 5972645
; GENERAL INFORMATION:

; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary L.
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; MOLECULES, AND USES THEREOF
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,211C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-211C-65

Query Match 2.6%; Score 8; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
| | | | |
Db 1 VLIVLAVI 8

RESULT 7

US-08-906-769-65
; Sequence 65, Application US/08906769
; Patent No. 6077687
; GENERAL INFORMATION:

; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,769
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,075
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-906-769-65

Query Match 2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
| | | | |
Db 1 VLIVLAVI 8

RESULT 8

US-08-906-616-65
; Sequence 65, Application US/08906616
; Patent No. 6121035
; GENERAL INFORMATION:

; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.

```
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,616
; FILING DATE: 05-AUG-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-906-616-65

Query Match      2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      252 VLIVLAVI 259
DB      1 VLIVLAVI 8

RESULT 9
US-08-817-795-65
; Sequence 65, Application US/08817795
; Patent No. 6139840
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Frank, Glenn R.
; APPLICANT: Heath, Andrew W.
; APPLICANT: Yamaka, Miles Yamanaka
; APPLICANT: Arfsten, Ann
; APPLICANT: Dale, Beverly
; APPLICANT: Stiegler, Gary
; TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
; TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
; TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, AND USES THEREOF
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Sheridan Ross & McIntosh
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,795
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14442
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gary J. Connell
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-817-795-65

Query Match      2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      252 VLIVLAVI 259
DB      1 VLIVLAVI 8

RESULT 10
US-08-485-443B-65
; Sequence 65, Application US/08485443B
; Patent No. 6146870
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary L.
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: SHERIDAN ROSS
; STREET: 1700 LINCOLN ST., SUITE 3500
; CITY: DENVER
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,443B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary L.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303 863-9700
; TELEFAX: 303 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-443B-65

Query Match      2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAVI 259
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Db 1 VLIVLAVI 8

RESULT 11

US-08-639-075A-65
; Sequence 65, Application US/08639075A
; Patent No. 6150125
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,075A
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-639-075A-65

Query Match 2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAVI 259
| | | | |
Db 1 VLIVLAVI 8

RESULT 12

US-09-012-431-65
; Sequence 65, Application US/09012431
; Patent No. 6180383
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.

; Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,431
; FILING DATE: 23-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,075
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-012-431-65

Query Match 2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAVI 259
| | | | |
Db 1 VLIVLAVI 8

RESULT 13

US-09-012-692-65
; Sequence 65, Application US/09012692
; Patent No. 6214579
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,692
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,075
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-012-692-65

Query Match 2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
DB 1 VLIVLAVI 8

RESULT 14
US-08-906-613-65
; Sequence 65, Application US/08906613
; Patent No. 6232096
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,075
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
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; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-906-613-65

Query Match 2.6%; Score 8; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
DB 1 VLIVLAVI 8

RESULT 15
PCT-US95-14442A-65
; Sequence 65, Application PC/TUS9514442A
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Frank, Glenn R.
; APPLICANT: Heath, Andrew W.
; APPLICANT: Yamaka, Miles Yamanaka
; APPLICANT: Arfsten, Ann
; APPLICANT: Dale, Beverly
; APPLICANT: Stiegler, Gary
; TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
; TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
; TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, AND USES THEREOF
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14442A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gary J. Connell
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; MOLECULE TYPE: protein
PCT-US95-14442A-65

Query Match 2.6%; Score 8; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
DB 1 VLIVLAVI 8
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Db 1 VLIIVLAVI 8

Search completed: June 15, 2004, 11:13:22
Job time : 17.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:10:00 ; Search time 39 Seconds
(without alignments)
2239.361 Million cell updates/sec

Title: US-09-524-531c-13
Perfect score: 310
Sequence: 1 MALRRRLRLRLVLRPHFL.....VNIRTSEGDPRHKSSFVI 310

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Gapop 60.0 , Gapext 60.0

Searched: 1158786 seqs, 281726120 residues

Word size : 0
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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published Applications AA:*
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12: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	7.7	238	15	US-10-410-842A-18
2	24	7.7	310	9	US-09-909-320-423
3	24	7.7	310	9	US-09-909-088B-423
4	24	7.7	310	9	US-09-905-291A-423
5	24	7.7	310	9	US-09-902-853-423
6	24	7.7	310	9	US-09-907-824-423
7	24	7.7	310	9	US-09-907-841-423
8	24	7.7	310	10	US-09-904-011-423
9	24	7.7	310	10	US-09-906-742-423
10	24	7.7	310	10	US-09-906-838-423
11	24	7.7	310	10	US-09-907-613-423
12	24	7.7	310	10	US-09-907-942-423
13	24	7.7	310	10	US-09-904-859-423
14	24	7.7	310	10	US-09-909-204-423
15	24	7.7	310	10	US-09-904-820-423

16	24	7.7	310	10	US-09-904-786-423	Sequence 423, App
17	24	7.7	310	10	US-09-906-646-423	Sequence 423, App
18	24	7.7	310	10	US-09-906-700-423	Sequence 423, App
19	24	7.7	310	10	US-09-903-786-423	Sequence 423, App
20	24	7.7	310	10	US-09-902-903-423	Sequence 423, App
21	24	7.7	310	10	US-09-903-749A-423	Sequence 423, App
22	24	7.7	310	10	US-09-904-119-423	Sequence 423, App
23	24	7.7	310	10	US-09-904-956-423	Sequence 423, App
24	24	7.7	310	10	US-09-902-736-423	Sequence 423, App
25	24	7.7	310	10	US-09-907-794-423	Sequence 423, App
26	24	7.7	310	10	US-09-903-943-423	Sequence 423, App
27	24	7.7	310	10	US-09-904-462-423	Sequence 423, App
28	24	7.7	310	10	US-09-907-925-423	Sequence 423, App
29	24	7.7	310	10	US-09-902-692-423	Sequence 423, App
30	24	7.7	310	10	US-09-903-520-423	Sequence 423, App
31	24	7.7	310	10	US-09-905-056-423	Sequence 423, App
32	24	7.7	310	10	US-09-909-064-423	Sequence 423, App
33	24	7.7	310	10	US-09-904-553-423	Sequence 423, App
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35	24	7.7	310	10	US-09-905-088-423	Sequence 423, App
36	24	7.7	310	10	US-09-907-575-423	Sequence 423, App
37	24	7.7	310	10	US-09-905-075-423	Sequence 423, App
38	24	7.7	310	10	US-09-902-759-423	Sequence 423, App
39	24	7.7	310	10	US-09-902-634-423	Sequence 423, App
40	24	7.7	310	10	US-09-902-713-423	Sequence 423, App
41	24	7.7	310	10	US-09-907-979-423	Sequence 423, App
42	24	7.7	310	10	US-09-902-615-423	Sequence 423, App
43	24	7.7	310	10	US-09-903-925-423	Sequence 423, App
44	24	7.7	310	10	US-09-906-760A-423	Sequence 423, App
45	24	7.7	310	10	US-09-903-823-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-10-410-842A-18
; Sequence 18, Application US/10410842A
; Publication No. US20030236396A1
; GENERAL INFORMATION:
; APPLICANT: Fasel et al
; TITLE OF INVENTION: SECRETORY SIGNAL SEQUENCES AND USES THEREOF
; FILE REFERENCE: 29964/37635A
; CURRENT APPLICATION NUMBER: US/10/410,842A
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/371,029
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-842A-18

Query Match 7.7%; Score 24; DB 15; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 167 PRPHYSWRNDVPLPTDSRANPRP 190
Db 167 PRPHYSWRNDVPLPTDSRANPRP 190
|||||

RESULT 2
US-09-909-320-423
; Sequence 423, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deansoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: KJavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/309,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-320-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
167 PRPHYSWYRNDVPLPDTSDRANPRF 190
|||||

Db 167 PRPHYSWYRNDVPLPDTSDRANPRF 190

RESULT 3
US-09-909-088B-423
Sequence 423, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: KJavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/309,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423

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; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-088B-423

Query Match          7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYNDVPLPTDSRANPRF 190
Db 167 PRPHYSWYNDVPLPTDSRANPRF 190

RESULT 4
US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-423

Query Match          7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYNDVPLPTDSRANPRF 190
Db 167 PRPHYSWYNDVPLPTDSRANPRF 190

RESULT 5
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-902-853-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVLPDTSRANPRF 190
Db 167 PRPHYSWRNDVLPDTSRANPRF 190

RESULT 6

US-09-907-824-423
; Sequence 423, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824

;; CURRENT FILING DATE: 2001-07-17
;; PRIOR APPLICATION NUMBER: 09/665,350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-824-423

Query Match 7.7%; Score 24; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVLPDTSRANPRF 190
Db 167 PRPHYSWRNDVLPDTSRANPRF 190

RESULT 7

US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,841

PRIOR FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 423

LENGTH: 310

TYPE: PRT

ORGANISM: Homo Sapien

US-09-907-841-423

Query Match 7.7%; Score 24; DB 9; Length 310;

Best Local Similarity 100.0%; Pred. No. 5.4e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANRP 190

DB 167 PRPHYSWYRNDVPLPTDSRANRP 190

RESULT 8

US-09-904-011-423

Sequence 423, Application US/09904011

Publication No. US2003003530A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary B.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Ashkenazi, Avi

APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,011

PRIOR FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 423

LENGTH: 310

TYPE: PRT

ORGANISM: Homo Sapien

US-09-904-011-423

Query Match 7.7%; Score 24; DB 10; Length 310;

Best Local Similarity 100.0%; Pred. No. 5.4e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANRP 190

DB 167 PRPHYSWYRNDVPLPTDSRANRP 190

RESULT 9

US-09-906-742-423

Sequence 423, Application US/09906742

Publication No. US20030023054A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANRP 190
|||||
Db 167 PRPHYSWYRNDVPLPTDSRANRP 190

RESULT 11

US-09-907-613-423
; Sequence 423, Application US/09907613
; Publication No. US20030027145A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613

; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-423

Query Match 7.7%; Score 24; DB 10; Length 310;

Best Local Similarity 100.0%; Pred. No. 5.4e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANRP 190
|||||
Db 167 PRPHYSWYRNDVPLPTDSRANRP 190

RESULT 12

US-09-907-942-423

; Sequence 423, Application US/09907942

; Publication No. US20030027146A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVPLTDSRANPRF 190
|||||
Db 167 PRPHYSWRNDVPLTDSRANPRF 190

RESULT 13
US-09-904-859-423
; Sequence 423, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWRNDVPLTDSRANPRF 190
|||||
Db 167 PRPHYSWRNDVPLTDSRANPRF 190

RESULT 14
US-09-909-204-423
; Sequence 423, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,204
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-204-423

Query Match 7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 PRPHSWYRNDVPLPTDSRANPRF 190
DB 167 PRPHSWYRNDVPLPTDSRANPRF 190

RESULT 15
US-09-904-820-423

Sequence 423, Application US/09904820
Publication No. US20030036094A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
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APPLICANT: Grimaldi, Christopher J.
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APPLICANT: Hillan, Kenneth, J.
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APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,820
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:06:35 ; Search time 14 Seconds
(without alignments)
2129.955 Million cell updates/sec

Title: US-09-524-531c-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLVLRPHFL.....VNYRTSRGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.6	146	2 F70313	hypothetical prote
2	8	2.6	204	2 A89919	conserved hypotet
3	8	2.6	208	2 D83431	type III export pr
4	8	2.6	506	2 T02400	probable beta-gluc
5	8	2.6	959	2 B85276	hypothetical prote
6	7	2.3	118	1 GLYC	gene 1 protein - S
7	7	2.3	128	2 C83448	succinate dehydrog
8	7	2.3	137	2 B41047	exsB protein - Pse
9	7	2.3	137	2 B83433	exoenzyme S synthe
10	7	2.3	173	2 B90241	hypothetical prote
11	7	2.3	177	2 B85833	partial probable s
12	7	2.3	177	2 B90988	partial probable s
13	7	2.3	194	2 T28889	hypothetical prote
14	7	2.3	208	2 T03627	GRP-binding protei
15	7	2.3	208	2 T01588	GRP-binding protei
16	7	2.3	214	2 T47268	phosphatidylserine
17	7	2.3	224	2 D71915	hydrogenase, cyto
18	7	2.3	232	2 S60984	hypothetical prote
19	7	2.3	246	2 F91238	PTS system, fructo
20	7	2.3	246	2 B86086	PTS system, fructo
21	7	2.3	249	2 G84224	hypothetical prote
22	7	2.3	255	2 B72474	hypothetical prote
23	7	2.3	267	2 B83705	phosphonates trans
24	7	2.3	269	1 C69651	prolipo protein dia
25	7	2.3	280	2 B83623	probable chemotaxi
26	7	2.3	287	2 E75159	hypothetical prote
27	7	2.3	322	2 B69009	cation antiporter
28	7	2.3	324	2 T27302	hypothetical prote
29	7	2.3	332	1 DEBYG1	glyceraldehyde-3-p

30 7 2.3 332 1 DEBYG2
31 7 2.3 332 2 C72485
32 7 2.3 335 2 S29813
33 7 2.3 337 2 A12360
34 7 2.3 348 2 B84143
35 7 2.3 359 2 H65201
36 7 2.3 380 2 H75159
37 7 2.3 387 2 E90533
38 7 2.3 402 2 G83367
39 7 2.3 421 2 H86217
40 7 2.3 422 2 D70110
41 7 2.3 429 2 AG2718
42 7 2.3 429 2 C97500
43 7 2.3 445 2 S75859
44 7 2.3 452 2 A70389
45 7 2.3 473 2 T28118

glyceraldehyde-3-p
probable high-affi
glyceraldehyde-3-p
hypothetical prote
L-iditol 2-dehydro
pts system, fructo
3-isopropylmalate
nitrogen fixation
hypothetical prote
protein 127G7.16 (a
aminotransferase (c
MFS permease [impo
hypothetical prote
hypothetical prote
L-seryl-tRNA^{Sec} se
hypothetical prote

ALIGNMENTS

RESULT 1
F70313
hypothetical protein aq_142 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000
C:Accession: F70313
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70313
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-146 <AQF>
A:Cross-references: GB:AE000675; NID:g2982863; PIDN:AAC06501.1; PID:g2982881; GB:AE0006
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_142
C:Superfamily: Aquifex aeolicus hypothetical protein aq_142

Query Match 2.6% Score 8; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLIVLAVI 259
Db 5 VLIVLAVI 12

RESULT 2
A89919
conserved hypothetical protein SA1250 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Jun-2003
C:Accession: A89919
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89919
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701215; PIDN:BA842510.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1250
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain ho

Query Match 2.6%; Score 8; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 IAGIIGGV 249
|||||
Db 181 IAGIIGGV 198

RESULT 3
T02400
type III export protein Peck PA1724 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83431
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A:Reference number: A82950; PMID:20437337; PMID:10984043
A:Accession: D83431
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-208 <STO>
A:Cross-references: GB:AE004598; GB:AE004091; NID:G9947687; PIDN:AAG05113.1; GSPDB:GN00140
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: peck; PA1724

Query Match 2.6%; Score 8; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRRLRLRL 11
|||||
Db 160 SRRLRLRL 167

RESULT 4
T02400
probable beta-glucosidase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C:Accession: T02400; F84878
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; PMID:20083487; PMID:10617197
A:Accession: F84878
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <STO>
A:Cross-references: GB:AE002093; NID:G3128187; PIDN:AAC16091.1; GSPDB:GN00139
C:Genetics:
A:Gene: F411.26; At2g44450
A:Map position: 2
A:Intron: 50/3; 74/1; 93/3; 119/1; 145/1; 174/2; 259/3; 370/1; 380/3; 415/1; 447/2
C:Superfamily: Agrobacterium beta-glucosidase

Query Match 2.6%; Score 8; DB 2; Length 506;

Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LVVLIVLA 257
|||||
Db 9 LVVLIVLA 16

RESULT 5
E85276
hypothetical protein AT4g24020 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: E85276
R:Anonymous, The European Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory
Nature 402, 763-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; PMID:20083488; PMID:10617198
A:Accession: E85276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-959 <STO>
A:Cross-references: GB:NC_001268; NID:G7269251; PIDN:CAB81320.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g24020
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical protein F23E12.170

Query Match 2.6%; Score 8; DB 2; Length 959;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 EAVNLKSS 37
|||||
Db 300 EAVNLKSS 307

RESULT 6
GLYC
gene 1 protein - Synecococcus sp. (strain PCC 6301)
C:Species: Synecococcus sp.
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S10825
R:Cosens, A.L.; Walker, J.B.
J. Mol. Biol. 194, 359-383, 1987
A:Title: The organization and sequence of the genes for ATP synthase subunits in the cytoplasm of Synecococcus sp.
A:Reference number: S07286; PMID:87311713; PMID:3041005
A:Accession: S10825
A:Molecule type: DNA
A:Residues: 1-118 <CO2>
A:Cross-references: EMBL:X05302; NID:G48009; PIDN:CAA28922.1; PID:G48011
C:Superfamily: gene 1 protein
C:Keywords: membrane protein

Query Match 2.3%; Score 7; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VVLIVLA 257
|||||
Db 75 VVLIVLA 81

RESULT 7
C83448
succinate dehydrogenase (C subunit) PA1581 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83448
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: C83448
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-128 <STO>
A:Cross-references: GB:AE004596; GB:AE004091; NID:g9947536; PIDN:AAG04970.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
C:Superfamily: succinate dehydrogenase 14K hydrophobic protein

Query Match 2.3%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 VVLIVLA 257
DB 117 VVLIVLA 123

RESULT 8
B41047
exsB protein - *Pseudomonas aeruginosa*
C:Species: *Pseudomonas aeruginosa*
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 08-Oct-1999
A:Accession: B41047
R:Frank, D.W.; Igilewski, B.H.
J. Bacteriol. 173, 6460-6468, 1991
A:Title: Cloning and sequence analysis of a trans-regulatory locus required for exoenzyme
A:Reference number: A41047; MUID:92011420; PMID:1655713
A:Accession: B41047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <FRA>
A:Cross-references: GB:M64975; NID:gl51217; PIDN:AA25815.1; PID:gl51219
C:Superfamily: *Pseudomonas aeruginosa* exsB protein

Query Match 2.3%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LRLRLYA 13
DB 41 LRLRLYA 47

RESULT 9
E83433
exoenzyme S synthesis protein B PA1712 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
A:Accession: E83433
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: E83433
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <STO>
A:Cross-references: GB:AE004597; GB:AE004091; NID:g9947671; PIDN:AAG05101.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
C:Superfamily: *Pseudomonas aeruginosa* exsB protein

Query Match 2.3%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LRLRLYA 13
DB 41 LRLRLYA 47

RESULT 10
B90241
hypothetical protein SSO0903 [imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
A:Accession: B90241
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, V.; Allard, G.; Aways, M.J.; Chan,
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I.;
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: B90241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-173 <KUR>
A:Cross-references: GB:AE006641; NID:gl3814083; PIDN:AAK41185.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO0903

Query Match 2.3%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 IIGGVLV 251
DB 102 IIGGVLV 108

RESULT 11
E85833
partial probable sensor kinase Z3235 [imported] - *Escherichia coli* (strain O157:H7, sub
partial probable sensor kinase Z3235 [imported])
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
A:Accession: E85833
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: E85833
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <STO>
A:Cross-references: GB:AE005174; NID:gl2516269; PIDN:AAG57129.1; GSPDB:GN00145; UWGP:Z3;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3235

Query Match 2.3%; Score 7; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 GGVLLVL 253
DB 139 GGVLLVL 145

RESULT 12
B90988
partial probable sensor kinase ECe2874 [similarity] - *Escherichia coli* (strain O157:H7,
partial probable sensor kinase ECe2874 [similarity])
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
A:Accession: B90988
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gawakara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene

A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <HAY>
A;Cross-references: PIDN:BA836297.1; PID:gl3362343; GSPDB:GN00154
A;Experimental source: strain O15:H7, substrain RMD 0509952
C;Genetics:
A;Gene: BCa2874

Query Match 2.3%; Score 7; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 GGVLVWL 253
|||||
Db 139 GGVLVWL 145

RESULT 13

T28889
hypothetical protein T14B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T28889

R;Favella, T.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid T14B4.
A;Reference number: Z20539
A;Accession: T28889
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-194 <FAV>
A;Cross-references: EMBL:U50191; PIDN:AAA91238.1; CESP:T14B4.5
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T14B4.5
A;Introns: 49/2; 104/2; 137/3
C;Superfamily: Caenorhabditis elegans hypothetical protein T14B4.5

Query Match 2.3%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLVVLAV 258
|||||
Db 93 VLVVLAV 99

RESULT 14

T03627
GTP-binding protein Rab6 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C;Accession: T03627
R;Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
Plant Physiol. 108, 59-67, 1995
A;Title: Characterization of membrane-bound small GTP-binding proteins from Nicotiana tabacum
A;Reference number: Z14896; MUID:95303981; PMID:7784525
A;Accession: T03627
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-208 <HA1>
A;Cross-references: EMBL:L29273; NID:g623585; PIDN:AAA74117.1; PID:g623586
A;Experimental source: strain SR1
C;Genetics:
A;Gene: Rab6

C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
P;10-125/Domain: translation elongation factor Tu homology <STU>
P;16-23/Region: nucleotide-binding motif A (P-loop)
P;122-125/Region: GTP-binding NKXD motif
P;152-154/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNLKSSN 38
|||||
Db 187 VNLKSSN 193

RESULT 15

T01588
GTP-binding protein At2g44610 - Arabidopsis thaliana
N;Alternate names: protein F16B22.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Mar-2001
C;Accession: T01588; F84880
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.
A;Reference number: Z14284
A;Accession: T01588
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-208 <ROU>

A;Cross-references: EMBL:AC003672; NID:g3341671; PIDN:AAC27463.1; PID:g3341681
A;Experimental source: Cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84880
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: GB:AE002093; NID:g3341681; PIDN:AAC27463.1; GSPDB:GN00139
C;Genetics:
A;Gene: F16B22.10; At2g44610
A;Map position: 2
A;Introns: 39/3; 63/2; 93/1; 130/2; 160/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
P;10-125/Domain: translation elongation factor Tu homology <STU>
P;16-23/Region: nucleotide-binding motif A (P-loop)
P;122-125/Region: GTP-binding NKXD motif
P;152-154/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNLKSSN 38
|||||
Db 187 VNLKSSN 193

Search completed: June 15, 2004, 11:12:36
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:05:10 ; Search time 10 Seconds
(without alignments)
1614.175 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYLPHLPFL.....VNYIRTSEGDPRKSKSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.6	146	Y142_AQUAE	O66537 aquifex aeo
2	7	2.3	118	ATP2_SYN6	P08443 synchococc
3	7	2.3	137	EXSB_PSEAE	P26994 pseudomonas
4	7	2.3	224	XLRI_MOUSE	Q92114 mus musculus
5	7	2.3	232	Y021_YEAST	Q99210 saccharomyc
6	7	2.3	269	LGT_BACSU	Q34752 bacillus su
7	7	2.3	280	CHR2_PSEAE	Q916V7 pseudomonas
8	7	2.3	331	G3P2_YEAST	P00358 saccharomyc
9	7	2.3	331	G3P3_YEAST	P00359 saccharomyc
10	7	2.3	335	G3P1_TRIKO	P17729 trichoderma
11	7	2.3	359	PTWC_ECOLI	P32672 escherichia
12	7	2.3	374	RL4_TRYBB	P49669 trypanosoma
13	7	2.3	380	LE22_PVRAB	Q9V1J0 pyrococcus
14	7	2.3	387	SRB2_HUMAN	Q9P1W8 homo sapien
15	7	2.3	422	CSD_FORBU	O51111 borrelia bu
16	7	2.3	452	SELA_AQUAE	O67140 aquifex aeo
17	7	2.3	473	YS81_CAEEL	Q09621 caenorhabdi
18	7	2.3	491	CPB4_RABIT	P00178 oryctolagus
19	7	2.3	491	CPB5_RABIT	P12789 oryctolagus
20	7	2.3	501	C6AH_DROME	Q9V770 drosophila
21	7	2.3	502	C6AN_DROME	Q9V771 drosophila
22	7	2.3	505	NDHF_BACSU	P39755 bacillus su
23	7	2.3	515	ROCA_OCEIH	O8erf4 oceanobacil
24	7	2.3	515	SYM_BRUSE	O8yh17 bruceella me
25	7	2.3	515	SYM_BRUSU	P59078 bruceella su
26	7	2.3	574	IRL2_MOUSE	Q9era7 mus musculus
27	7	2.3	578	OXAA_PSEAE	Q9ht06 pseudomonas
28	7	2.3	586	HOLI_YEAST	P53389 saccharomyc
29	7	2.3	697	CEAD_ECOLI	P17998 escherichia
30	7	2.3	758	SC18_YEAST	P18759 saccharomyc
31	7	2.3	774	VP4_ROTHT	P11200 human rotav
32	7	2.3	775	VP4_ROTTH	P11197 human rotav
33	7	2.3	776	VP4_ROTTH	P11199 human rotav

34	7	2.3	805	1	YC26_METJA	Q58623 methanococc
35	7	2.3	806	1	AD1B_MOUSE	Q8r534 mus musculu
36	7	2.3	810	1	SYFB_ANASP	Q8ym55 anabaena sp
37	7	2.3	840	1	CC16_YEAST	P09798 saccharomyc
38	7	2.3	1105	1	YEGE_ECOLI	P38097 escherichia
39	7	2.3	1129	1	HPX5_HUMAN	Q9up23 homo sapien
40	7	2.3	1234	1	YXK5_CAEEL	P34578 caenorhabdi
41	7	2.3	2871	1	FBN1_BOVIN	P98133 bos taurus
42	7	2.3	2871	1	FBN1_HUMAN	P35555 homo sapien
43	7	2.3	2871	1	FBN1_MOUSE	Q61554 mus musculu
44	7	2.3	2871	1	FBN1_PIG	Q9tv36 sus scrofa
45	7	2.3	3014	1	CLRI_HUMAN	Q9nyq6 homo sapien

ALIGNMENTS

RESULT 1
Y142_AQUAE STANDARD; PRT; 146 AA.
ID Y142_AQUAE
AC O66537;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_142.
GN AQ_142.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL Nature 392:353-358(1998).

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CC -----
EMBL; AS000675; AAC06501.1; --
DR PIR; F70313; F70313.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 146 AA; 16321 MW; 9E98228A820CC2B2 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 252 VLIVLAVI 259
Db 5 VLIVLAVI 12
|||||

RESULT 2
ATP2_SYN6 STANDARD; PRT; 118 AA.
ID ATP2_SYN6
AC P08443;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase protein I.
GN ATP1.
OS Synchococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.

```

OX NCBI_TaxID=1139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87311713; PubMed=3041005;
RA Cozens A.L., Walker J.E.;
RT "The organization and sequence of the genes for ATP synthase subunits
RT in the cyanobacterium Synechococcus 6301. Support for an
RL endosymbiotic origin of chloroplasts.";
RL J. Mol. Biol. 194:359-383(1987).
CC -!- FUNCTION: A possible function for this protein is to guide the
CC assembly of the membrane sector of the ATPase enzyme complex.
CC -!- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.
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CC -----
DR EMBL; X05302; CAA28922.1; -.
DR PIR; S10825; GLYC.
KW Hydrogen ion transport; CF(0); Transmembrane.
PT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
SQ SEQUENCE 118 AA; 13455 MW; 16B76A47F76CC196 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Oy 251 VVLIVLA 257
Db 75 VVLIVLA 81

RESULT 3
EXSB_PSEAE STANDARD; PRT; 137 AA.
AC P26954;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Exoenzyme S synthesis protein B.
GN EXSB OR PA1712.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RC MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- SIMILARITY: TO Y. ENTEROCOLITICA VIRB.

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CC -----
DR EMBL; M64975; AAA25815.1; -.
DR EMBL; AE004597; AAG05101.1; -.
DR PIR; B41047; B41047.
DR PIR; E83433; E83433.
KW Complete proteome.
FT CONFLICT 62 62 R -> W (IN REF. 1).
SQ SEQUENCE 137 AA; 14996 MW; F7367E7AB301C4EA CRC64;

Query Match 2.3%; Score 7; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Oy 7 LRLRLYA 13
Db 41 LRLRLYA 47

RESULT 4
XLRL1_MOUSE STANDARD; PRT; 224 AA.
ID XLRL1_MOUSE
AC O921I4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Retinoschisin precursor (X-linked juvenile retinoschisis protein
DE homolog).
GN RS1 OR RSIH OR XLRS1.
OS Mus musculus (Mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SwJ;
RC MEDLINE=99160474; PubMed=10051329;
RA Gehrig A.B., Warneke-Wittstock R., Sauer C.G., Weber B.H.F.;
RT "Isolation and characterization of the murine X-linked juvenile
RT retinoschisis (Rslh) gene.";
RL Mamm. Genome 10:303-307(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CS7BL/6; TISSUE=Eye;
RC Brunner B., Todt T., Lenzner S., Stout K., Schulz U., Ropers H.-H.,
RA Kalscheuer V.M.;
RT "Genomic structure and comparative analysis of seven contiguous genes
RT disclose a large region with conserved gene order in human Xp22.2-
RT p22.1.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Retina;
RC MEDLINE=99148018; PubMed=10023077;
RA Reid S.N., Akhmedov N.B., Pivov N.I., Kozak C.A., Danciger M.,
RA Farber D.B.;
RT "The mouse X-linked juvenile retinoschisis cDNA: expression in
RT photoreceptors.";
RL Gene 227:257-266(1999).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Retina;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be active in cell adhesion processes during retinal
CC development (by similarity).
CC -!- TISSUE SPECIFICITY: Retinal specific.
CC -!- SIMILARITY: Contains 1 P5/8 type C domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF084561; AAD21808.1; -
DR EMBL; AF084567; AAD21809.1; -
DR EMBL; AF084562; AAD21809.1; JOINED.
DR EMBL; AF084563; AAD21809.1; JOINED.
DR EMBL; AF084564; AAD21809.1; JOINED.
DR EMBL; AF084565; AAD21809.1; JOINED.
DR EMBL; AF084566; AAD21809.1; JOINED.
DR EMBL; AJ011381; CAA09601.1; -
DR EMBL; BC046422; AAH46422.1; -
DR HSSP; P12259; 1C2T.
DR MGD; MGI:1336189; Rslh.
DR InterPro; IPR000421; PAS8 C.
DR InterPro; IPR008979; Gal_Bind like.
DR Pfam; PF00754; F5_P8 type C; 1.
DR SMART; SM00231; FA58C; 1.
DR PROSITE; PS01285; PAS8C.1; 1.
DR PROSITE; PS01286; PAS8C.2; FALSE_NRG.
DR PROSITE; PS50022; PAS8C_3; 1.
KW Cell adhesion; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 224 RETINOSCHISIN.
FT DOMAIN 63 219 F5/8 TYPE C.
FT DISULPID 63 219 BY SIMILARITY.
SQ SEQUENCE 224 AA; 25575 MW; 4536203CC00E90E4 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FFLLLLF 24
DB 8 FFLLLLF 14

RESULT 5
YOZ1_YEAST STANDARD; PRT; 232 AA.
AC Q99210;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Hypothetical protein YOR111W.

Query Match 2.3%; Score 7; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FFLLLLF 24
DB 8 FFLLLLF 14

RESULT 6
LGT_BACSU STANDARD; PRT; 269 AA.
ID LGT_BACSU
AC O34752;
DC 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) (Spore
DE germination protein gerP).
GN LGT OR GERF OR BSU34990.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN SEQUENCE FROM N.A.
RA Robinson C., Rivolta C., Karamata D., Moir A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN (2)

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GN YOR111W OR YOR3237W OR O3237.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97060020; PubMed=8904341;
RA Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vlcek C.,
RA Stegemann J., Zimmermann J., Erfle H., Paces V., Ansong W.;
RT "Sequencing and analysis of 51 kb on the right arm of chromosome XV
RT from Saccharomyces cerevisiae reveals 30 open reading frames.";
RN Yeast 12:281-288(1996).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE=97344368; PubMed=9200815;
RA Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,
RA Schwager C., Paces V., Sander C., Ansong W.;
RT "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
RN Yeast 13:655-672(1997).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the maf family.
CC -----
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CC -----
DR EMBL; X94335; CAA64031.1; -
DR EMBL; X90518; CAA62105.1; -
DR EMBL; Z75019; CAA99309.1; -
DR PIR; S60984; S60984.
DR HSSP; Q02169; 1EX2.
DR Germline; 143699; -.
DR SGD; S0005637; YOR111W.
DR InterPro; IPR003697; Maf.
DR Pfam; PF02545; Maf; 1.
DR TIGRFAMs; TIGR00172; maf; 1.
DR Hypothetical protein.
FT ACT_SITE 52 52 POTENTIAL.
SQ SEQUENCE 232 AA; 26477 MW; C0A83ED2AE20BE13 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VYFDNKI 84
DB 166 VYFDNKI 172

RESULT 6
LGT_BACSU STANDARD; PRT; 269 AA.
ID LGT_BACSU
AC O34752;
DC 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) (Spore
DE germination protein gerP).
GN LGT OR GERF OR BSU34990.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN SEQUENCE FROM N.A.
RA Robinson C., Rivolta C., Karamata D., Moir A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN (2)

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RP SEQUENCE FROM N.A.
RA Lazarevic V., Soldo B., Rivolta C., Reynolds S., Mauei C.,
RA Karamata D.;
RT "Nucleotide sequence of the 300-304 chromosomal segment of *Bacillus*
RT *subtilis*,"
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell I.B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.P., Itaya M., Jones L.,
RA Joris B., Karamata D., Kaahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauei C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone P.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yaeumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumschein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*,"
RL Nature 390:249-256(1997).
CC -1- FUNCTION: Transfers the N-acyl diglyceride group on what will
CC become the N-terminal cysteine of membrane lipoproteins.
CC -1- PATHWAY: Lipoproteins biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the lgt family.
CC
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CC
CC EMBL; AF017113; AAC67287.1; -
CC EMBL; Z99121; CAB15504.1; -
CC PIR; C69651; C69651.
CC Subtilist; BG12611; lgt.
CC InterPro; IPR001640; lgt.
CC Pfam; PF01790; lgt; 1.
CC ProDom; PD005412; lgt; 1.
CC TIGRfam; TIGR00544; lgt; 1.
CC PROSITE; PS01311; lgt; 1.
CC Transferrase; Transmembrane; Germination; Complete proteome.
CC TRANSMEM 18 38
CC TRANSMEM 52 72 POTENTIAL.
CC TRANSMEM 89 109 POTENTIAL.
CC TRANSMEM 116 136 POTENTIAL.
CC TRANSMEM 177 197 POTENTIAL.
CC TRANSMEM 205 225 POTENTIAL.
CC TRANSMEM 236 256 POTENTIAL.
CC SEQUENCE 269 AA; 30619 MW; 6D2E00DC07482C68 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 252 VLIVLAV 258
DB 245 VLIVLAV 251
|||||
RESULT 7
CHR2 PSBAE STANDARD; PRT; 280 AA.
ID Q16V77; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotaxis protein methyltransferase 2 (EC 2.1.1.80).
GN CHER2 OR PA0175.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz S.N., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING
CC RESIDUES IN MCP (BY SIMILARITY).
CC = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
CC -1- SIMILARITY: Contains 1 cheR-type methyltransferase domain.
CC
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CC
CC EMBL; AB004455; AAG03565.1; -
CC PIR; H83623; H83623.
CC HSSP; P07801; 1AF7.
CC InterPro; IPR000780; CheR Metranf.
CC Pfam; PF01703; CheR; 1.
CC Pfam; PF03705; CheR N; 1.
CC PRINTS; SM00396; CHERMTFRASE.
CC SMART; SM00138; Metrc; 1.
CC PROSITE; PS0123; CHER; 1.
CC TRANSFERASE; Methyltransferase; Complete proteome.
CC DOMAIN 10 280 CHER-TYPE METHYLTRANSFERASE.
CC SEQUENCE 280 AA; 32028 MW; FD2AF1491DDC57FB CRC64;
Query Match 2.3%; Score 7; DB 1; Length 280;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LSRRLRL 9
DB 49 LSRRLRL 55
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RESULT 8
G3P2 YEAST
ID G3P2 YEAST STANDARD; PRT; 331 AA.
AC P00358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase 2 (EC 1.2.1.12) (GAPDH 2).
GN TDH2 OR GPD2 OR YJR009C OR J1433.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=92160396; PubMed=1789010;
RA Mountain H.A., Korch C.;
RT "TDH2 is linked to MET3 on chromosome X of Saccharomyces cerevisiae.";
RL Yeast 7:873-880(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=80137492; PubMed=6244283;
RX Holland J.P., Holland M.J.;
RA "Structural comparison of two non-tandemly repeated yeast
RT glyceraldehyde-3-phosphate dehydrogenase genes.";
RL J. Biol. Chem. 255:2596-2605(1980).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1679;
RA de Haan M., Smits P.H.M., Grivell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCES OF 23-36; 71-76; 80-85; 198-212; 225-231 AND 321-330.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=95255188; PubMed=7737086;
RA Norbeck J., Blomberg A.;
RT "Gene linkage of two-dimensional polyacrylamide gel electrophoresis
RT resolved proteins from isogene families in Saccharomyces cerevisiae
RT by microsequencing of in-gel trypsin generated peptides.";
RL Electrophoresis 15:149-156(1995).
RN [5]
RP SEQUENCE OF 1-12.
RC STRAIN=X12 / W3110;
RA Frutiger S., Hughes G.J., Sanchez J.-C., Hochstrasser D.P.;
RL Submitted (FEB-1996) to Swiss-Prot.
CC -|- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -|- PATHWAY: Second phase of glycolysis; first step.
CC -|- SUBUNIT: Homotetramer.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- MISCELLANEOUS: THERE ARE THREE GENES FOR G3PDH IN YEAST.
CC -|- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC dehydrogenase family.
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DR EMBL; X60157; CA942725.1;
DR EMBL; V01301; CA9424608.1; ALT_SEQ.
DR EMBL; X87611; CA960931.1;
DR EMBL; Z49509; CA989531.1;
DR PIR; S57024; DEBYG1.
DR HSP; P06977; 1GAD.
DR GeneOnline; 141845;
DR SWISS-2DPAGE; P00358; YEAST.
DR COMPUYEAST-2DPAGE; P00358;
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DR SGD; S0003769; TDH2.
DR GO; GO:0005277; C:cell wall (sensu Fungi); IDA.
DR GO; GO:0005811; C:lipid particle; IDA.
DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IDA.
DR InterPro; IPR000173; GAP dhdrogenase.
DR InterPro; IPR006424; GAPDH-I.
DR Pfam; PF00044; gpdh; 1.
DR PRINTS; PR00078; G3PDHGRNASE.
DR TIGRPFAM; TIGR01534; GAPDH-I; 1.
DR PROSITE; PS00071; GAPDH; 1.
KW Glycolysis; Oxidoreductase; NAD; Multigene family.
PT INIT_MET 0
FT BINDING 149 149 GLYCERALDEHYDE 3-PHOSPHATE.
FT ACT_SITE 176 176 ACTIVATES THIOL GROUP DURING CATALYSIS.
FT CONFLICT 76 76 E -> A (IN REF. 4).
SQ SEQUENCE 331 AA; 35715 MW; 3998B6F655AFDFC4 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 331;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 EVVALND 122
DB 26 EVVALND 32
|||||

RESULT 9
G3P3 YEAST STANDARD; PRT; 331 AA.
ID G3P3 YEAST
AC P00359;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase 3 (EC 1.2.1.12) (GAPDH 3).
GN TDH3 OR GPD3 OR YGR192C OR G7576.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80027306; PubMed=385592;
RA Holland J.P., Holland M.J.;
RT "The primary structure of a glyceraldehyde-3-phosphate dehydrogenase
RT gene from Saccharomyces cerevisiae.";
RL J. Biol. Chem. 254:9839-9845(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c;
RX MEDLINE=95373283; PubMed=7645350;
RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez M.,
RA Nombela C.;
RT "The complete sequence of a 9037 bp DNA fragment of the right arm of
RT Saccharomyces cerevisiae chromosome VII.";
RL Yeast 11:587-591(1995).
RN [3]
RP SEQUENCE OF 46-57.
RC STRAIN=S288c;
RX MEDLINE=95203288; PubMed=7895733;
RA Carrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [4]
RP PARTIAL SEQUENCE.
RC STRAIN=ATCC 38531 / Y41, and ATCC 44827 / SKQ2N;
RX MEDLINE=95255188; PubMed=7737086;
RA Norbeck J., Blomberg A.;
RT "Gene linkage of two-dimensional polyacrylamide gel electrophoresis
RT resolved proteins from isogene families in Saccharomyces cerevisiae
RT by microsequencing of in-gel trypsin generated peptides.";
RN [5]
```


OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RT Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes.";
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [2]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=95291446; PubMed=7773398;
RA Reizer J., Reizer A., Sauer M.H. Jr.;
RT "Novel phosphotransferase system genes revealed by bacterial genome
RT analysis -- a gene cluster encoding a unique Enzyme I and the proteins
RT of a fructose-like permease system.";
RL Microbiology 141:961-971(1995).
CC -!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
CC sugar phosphotransferase system (PTS), a major carbohydrate active
CC and transport system. The IICD domains contain the sugar binding site
CC and the transmembrane channel; the IIA domain contains the primary
CC phosphorylation site (the donor is phospho-HPr); IIA transfers its
CC phosphoryl group to the IIB domain which finally transfers it to
CC the sugar.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Contains 1 PTS IIC domain.
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CC
DR EMBL; U00006; AAC43055.1; -;
DR EMBL; AE000469; AAC76931.1; -;
DR PIR; H65201; H65201.
DR EcoGene; EG11908; frcW.
DR InterPro; IPR003352; Ptrans IIC.
DR InterPro; IPR006327; PTS_IIC_fruct.
DR Pfam; PF02378; PTS_EIIC; 1.
DR TIGRFAMs; TIGR01427; PTS_IIC_fructo; 1.
KW Phosphotransferase system; Sugar transport; Transmembrane;
KW Inner membrane; Complete proteome.
FT TRANSMEM 19 39 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 216 236 POTENTIAL.
FT TRANSMEM 251 271 POTENTIAL.
FT TRANSMEM 290 310 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
SQ SEQUENCE 359 AA; 37086 MW; 1CB60AF9FF6CCDDAD CRC64;

Query Match 2.3%; Score 7; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IAGIIG 248
Db 108 IAGIIG 114
|||||
- - - - -
RESULT 12
RL4_TRYBB
ID - RL4_TRYBB STANDARD; PRT; 374 AA.
AC P49669;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE 60S ribosomal protein L4 (L1).
GN RPL4 OR RPL1.
OS Trypanosoma brucei brucei.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RA Wilson K., Uyetake L., Boothroyd J.C.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the L4B family of ribosomal proteins.
CC
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CC
DR EMBL; Z54340; CAA91141.1; -;
DR InterPro; IPR002136; Ribosomal_L4/L1E.
DR Pfam; PF00573; Ribosomal_L4; 1.
DR PROSITE; PS00939; RIBOSOMAL_L1E; 1.
KW Ribosomal protein.
SQ SEQUENCE 374 AA; 41886 MW; 67415135001F9804 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RLRLRL 11
Db 323 RLRLRL 329
|||||
- - - - -
RESULT 13
LE22_PYRAB
ID - LE22_PYRAB STANDARD; PRT; 380 AA.
AC Q9V1J0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit 2 (EC 4.2.1.33)
DE (Isopropylmalate isomerase 2) (Alpha-IPM isomerase 2) (IPMI 2).
GN LEUC2 OR PYRAB04370 OR PAB0287.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB5 / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RA Cohen G.N., Barbe V., Plament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissbach J., Zivanovic Y., Porterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate +
CC H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmaleate.
CC -!- COFACTOR: Binds 1 4Fe-4S cluster per subunit (By similarity).
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -!- SIMILARITY: Belongs to the aconitase/IPM isomerase family. Leuc 2
CC subfamily.
CC
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 CC -----

DR EMBL; AJ248284; CAB49359.1; -;
 DR PIR; H75159; H75159.
 DR HAMAP; MF 01027; -; 1.
 DR InterPro; IPR001030; Aconitase N.
 DR InterPro; IPR006251; Cis-H aconitase.
 DR Pfam; PF00330; aconitase; 1.
 DR PRINTS; PR00415; ACONITASE.
 DR ProDom; PD000511; Aconitase N; 1.
 DR TIGRFAMs; TIGR01343; haca_fam; 1.
 DR PROSITE; PS00450; ACONITASE 1; 1.
 DR PROSITE; PS01244; ACONITASE 2; 1.
 KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
 FT METAL 262 262 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 FT METAL 320 320 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 FT METAL 323 323 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 SQ SEQUENCE 380 AA; 41088 MW; B22E1E6D8016FAD CRC64;

Query Match 2.3%; Score 7; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 DEITIEL 133

Db 221 DEITIEL 227

RESULT 14

ID_SRB2 HUMAN STANDARD; PRT; 387 AA.
 AC QP1W8; Q8WNA5; Q9NQK8.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Signal-regulatory protein beta-2 precursor (SIRP-beta-2) (SIRP-b2).
 GN SIRPB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 (1)
 RP SEQUENCE FROM N.A. (ISOPFORM 2).
 RC TISSUE=Placenta;
 RX MEDLINE=2103165; PubMed=11185750;
 RA Ichigotani Y., Matsuda S., Machida K., Oshima K., Iwamoto T.,
 RA Yamaki K., Hayakawa T., Hamaguchi M.;
 RT "Molecular cloning of a novel human gene (SIRP-B2) which encodes a new
 RT member of the SIRP/SHPS-1 protein family.";
 RL J. Hum. Genet. 45:378-382(2000).
 (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,
 RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown N.P.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaaialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sahra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 (3)
 RP SEQUENCE FROM N.A. (ISOPFORM 3).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausberg R.D., Collins P.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Probable immunoglobulin-like cell surface receptor.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Rvent=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC Name=2;
 CC Name=3;
 CC IsoId=Q9PIW8-1; Sequence=Displayed;
 CC IsoId=Q9PIW8-2; Sequence=VSP_007027;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q9PIW8-3; Sequence=VSP_007028;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Detected in liver, and at very low levels in
 CC brain, heart, lung, pancreas, kidney, placenta and skeletal
 CC muscle.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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EMBL; AB042624; BA95692.1; -;
 EMBL; AL138804; CAC00474.1; -;
 EMBL; BC020629; ANH20629.1; ALT_INIT.
 Genew; HGNC:15757; SIRPB2.
 MIM; 605466; -;
 GO; GO:0007267; P:cell-cell signaling; TAS
 GO; GO:0007242; P:intracellular signaling cascade; TAS.
 GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003597; Ig cl.
 InterPro; IPR003006; Ig_MHC.

```
DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00447; ig_3.  
DR SMART: SM00407; Igc1; 2.  
DR SMART: SM00406; Igc1; 1.  
DR PROSITE: PS00835; IG LIKE; 3.  
DR PROSITE: PS00290; IG MHC; FALSE NEG.  
KW Repeat: Signal: Transmembrane; Immunoglobulin domain; Glycoprotein;  
KW Alternative splicing.  
FT SIGNAL 1 28  
FT CHAIN 29 387  
FT DOMAIN 29 360  
FT TRANSMEM 361 383  
FT DOMAIN 384 387  
FT DOMAIN 129 137  
FT DOMAIN 146 245  
FT DOMAIN 252 340  
FT DISULFID 53 119  
FT DISULFID 168 226  
FT DISULFID 271 329  
FT CARBOHYD 243 243  
FT CARBOHYD 268 268  
FT CARBOHYD 309 309  
FT CARBOHYD 317 317  
FT VARSPLIC 1 33  
FT VARSPLIC 144 360  
FT CONFLICT 263 263  
FT CONFLICT 286 286  
SQ SEQUENCE 387 AA; 42495 MW; P7F20C9F85E0E64B CRC64;  
  
Query Match 2.3%; Score 7; DB 1; Length 387;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 152 VCKTATL 158  
DB 45 VKTATL 51  
|||||  
  
RESULT 15  
CSD BORBU STANDARD; PRT; 422 AA.  
AC OS111;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Probable cysteine desulfurase (SC 4.4.1.-).  
GN CSD OR BB0084  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35210 / B31;  
RX MEDLINE=98065943; PubMed=9403685;  
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,  
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,  
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,  
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,  
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,  
RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,  
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,  
RA Smith H.O., Venter J.C.;  
RT "Genomic sequence of a Lyme disease spirochete, Borrelia  
RT burgdorferi";  
RL Nature 390:580-586(1997).  
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur and selenium  
CC atoms from L-cysteine, L-cystine, L-selenocysteine, and L-  
CC selenocystine to produce L-alanine (By similarity).  
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -!- SIMILARITY: Belongs to class-v of pyridoxal-phosphate-dependent  
CC aminotransferases. Csd subfamily.
```

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CC -----  
DR EMBL; AE001121; AAC66472.1; -.  
DR PIR; D70110; D70110.  
DR HSSP; P77444; 1JF9.  
DR TIGR; BR0084; -.  
DR InterPro: IPR000192; Aminotrans_v.  
DR Pfam; PF00266; aminotran_5; 1.  
DR PROSITE; PS00595; AA_TRANSF_CLASS_5; 1.  
KW Lyase; Pyridoxal phosphate; Complete proteome.  
FT BINDING 235 235 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SQ SEQUENCE 422 AA; 48124 MW; 0D37CE39059C2EDD CRC64;  
  
Query Match 2.3%; Score 7; DB 1; Length 422;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 241 NIAGIIG 247  
DB 292 NIAGIIG 298  
|||||  
  
Search completed: June 15, 2004, 11:10:30  
Job time : 11 secs
```

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OM protein -- protein search, using sw model

Run on: June 15, 2004, 11:05:50 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRLRLRLYLRLPHPL.....VNYRTSEGGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL.25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	253	81.6	310	11	Q9EPK4	Q9EPK4 mus musculu
2	245	79.0	310	11	Q9D1M9	Q9D1M9 mus musculu
3	152	49.0	310	11	Q9D8B7	Q9D8B7 mus musculu
4	64	20.6	64	11	Q8BT59	Q8BT59 mus musculu
5	24	7.7	309	4	Q96FL1	Q96FL1 homo sapien
6	24	7.7	310	4	Q9BX67	Q9BX67 homo sapien
7	24	7.7	355	4	Q8WNL8	Q8WNL8 homo sapien
8	8	2.6	92	2	Q8RCQ2	Q8RCQ2 bacillus ce
9	8	2.6	131	5	Q81RS1	Q81RS1 anopheles g
10	8	2.6	165	12	Q8AZH5	Q8AZH5 rabbit hemo
11	8	2.6	204	16	Q99U70	Q99U70 staphylococ
12	8	2.6	204	16	Q8NWR5	Q8NWR5 staphylococ
13	8	2.6	204	16	Q8CSL1	Q8CSL1 staphylococ
14	8	2.6	206	2	P95439	P95439 pseudomonas
15	8	2.6	208	16	Q91313	Q91313 pseudomonas
16	8	2.6	215	16	Q81R03	Q81R03 bacillus an

17	8	2.6	215	16	Q81DY6	Q81DY6 bacillus ce
18	8	2.6	246	5	Q9XY46	Q9XY46 entamoeba h
19	8	2.6	317	5	Q818D9	Q818D9 corynebacte
20	8	2.6	324	16	Q8NLA6	Q8NLA6 arabisidopsi
21	8	2.6	400	10	Q9LT44	Q9LT44 arabisidopsi
22	8	2.6	443	16	Q7WIH9	Q7WIH9 bordetella
23	8	2.6	443	16	Q7W6K5	Q7W6K5 bordetella
24	8	2.6	443	16	Q7VYK6	Q7VYK6 bordetella
25	8	2.6	462	16	Q8XXW0	Q8XXW0 cistridium
26	8	2.6	506	10	Q64879	Q64879 arabisidopsi
27	8	2.6	959	10	Q22987	Q22987 arabisidopsi
28	8	2.6	959	10	Q84TH9	Q84TH9 arabisidopsi
29	8	2.6	1005	5	Q8RTM0	Q8RTM0 bombyx mori
30	8	2.6	1065	16	Q81BF4	Q81BF4 bacillus ce
31	7	2.3	65	5	Q81AB5	Q81AB5 caenorhabdi
32	7	2.3	67	4	Q8NI85	Q8NI85 homo sapien
33	7	2.3	68	2	Q8GAP5	Q8GAP5 arthroacte
34	7	2.3	85	9	Q8SC57	Q8SC57 stx2 conver
35	7	2.3	85	9	Q7Y345	Q7Y345 stx1 conver
36	7	2.3	85	9	Q7Y2N4	Q7Y2N4 stx2 conver
37	7	2.3	85	12	Q99GX8	Q99GX8 helicoverpa
38	7	2.3	92	10	Q8LFP4	Q8LFP4 arabisidopsi
39	7	2.3	92	10	Q8GXY9	Q8GXY9 arabisidopsi
40	7	2.3	95	10	Q9FE08	Q9FE08 perilla fru
41	7	2.3	115	12	Q7TFD7	Q7TFD7 rhesus cyto
42	7	2.3	121	2	Q93HQ4	Q93HQ4 streptococc
43	7	2.3	126	16	Q89H27	Q89H27 bradyrhizob
44	7	2.3	128	16	Q913D7	Q913D7 pseudomonas
45	7	2.3	133	16	Q83AG2	Q83AG2 coxiella bu

ALIGNMENTS

RESULT 1

Q9EPK4	PRELIMINARY;	PRT;	310 AA.
ID	Q9EPK4		
AC	Q9EPK4;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)		
DE	(Junctional cell adhesion molecule 3).		
GN	JAM3 OR JCM3 OR JCM2 OR JAM-2 OR 1110002N23Rik.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=11036763;		
RT	Aurand-Lions M.A., Duncan L., Du Pasquier L., Inhof B.A.;		
RT	"Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular		
RT	Family?";		
RL	Curr. Top. Microbiol. Immunol. 251:91-98 (2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CS7BL/6J; TISSUE=Embryo;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RC MEDLINE=22354683; PubMed=12466851;
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RC MEDLINE=22354683; PubMed=12466851;
RC TISSUE=Kidney;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AJ300304; CAC20704.1; -;
DR EMBL; AK013156; BAB28683.1; -;
DR EMBL; BC024357; AAB24357.1; -;
DR EMBL; AK032833; BAC28049.1; -;
DR MGD; MGI:1933825; Jam3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR SMART; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;

Query Match 81.6%; Score 253; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. NO. 1e-264;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 SQTSDPRIWKIKIQDQTTVYFQNKIQGLAGRTDVFQKTSLRINWVTRSDSAIYRCEV 117
Db |||||||
Qy 58 SQTSDPRIWKIKIQDQTTVYFQNKIQGLAGRTDVFQKTSLRINWVTRSDSAIYRCEV 117
Db |||||||
Qy 118 VALNDRKVEDEITIELIVQVKPVPVCRIPAAVPGVGTATLQCESSEGYPRPHYSWYRND 177
Db |||||||
Qy 118 VALNDRKVEDEITIELIVQVKPVPVCRIPAAVPGVGTATLQCESSEGYPRPHYSWYRND 177
Db |||||||
Qy 178 VPLPTDSRANPRFQNSFFHVNSETGLVFNVAHVHDDSGQYICIASNDAGAARCEGQDMEV 237
Db |||||||
Qy 178 VPLPTDSRANPRFQNSFFHVNSETGLVFNVAHVHDDSGQYICIASNDAGAARCEGQDMEV 237
Db |||||||
Qy 238 YDLNIAGIIGVLVVLIVLAVITWGICCAVRRGCFISSKQDGSYKSPGKHGWNVYIRTS 297
Db |||||||
Qy 238 YDLNIAGIIGVLVVLIVLAVITWGICCAVRRGCFISSKQDGSYKSPGKHGWNVYIRTS 297
Db |||||||
Qy 298 EBGDFRHKSPFI 310
Db |||||||
Qy 298 EBGDFRHKSPFI 310
Db |||||||

RESULT 2
Q9D1M9 PRELIMINARY; PRT; 310 AA.
AC Q9D1M9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai J., Offord T., Furuno M., Anon H., Baldarelli R., Barsh G.,
RA Blake K., Roffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaeris P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003326; BAB22715.1; -;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR SMART; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 79.0%; Score 245; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. NO. 4.5e-256;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 SQTSDPRIWKIKIQDQTTVYFQNKIQGLAGRTDVFQKTSLRINWVTRSDSAIYRCEV 117
Db |||||||
Qy 58 SQTSDPRIWKIKIQDQTTVYFQNKIQGLAGRTDVFQKTSLRINWVTRSDSAIYRCEV 117
Db |||||||
Qy 118 VALNDRKVEDEITIELIVQVKPVPVCRIPAAVPGVGTATLQCESSEGYPRPHYSWYRND 177
Db |||||||
Qy 118 VALNDRKVEDEITIELIVQVKPVPVCRIPAAVPGVGTATLQCESSEGYPRPHYSWYRND 177
Db |||||||
Qy 178 VPLPTDSRANPRFQNSFFHVNSETGLVFNVAHVHDDSGQYICIASNDAGAARCEGQDMEV 237
Db |||||||
Qy 178 VPLPTDSRANPRFQNSFFHVNSETGLVFNVAHVHDDSGQYICIASNDAGAARCEGQDMEV 237
Db |||||||
Qy 238 YDLNIAGIIGVLVVLIVLAVITWGICCAVRRGCFISSKQDGSYKSPGKHGWNVYIRTS 297
Db |||||||
Qy 238 YDLNIAGIIGVLVVLIVLAVITWGICCAVRRGCFISSKQDGSYKSPGKHGWNVYIRTS 297
Db |||||||
Qy 298 EBGDF 302
Db |||||||
Qy 298 EBGDF 302
Db |||||||

RESULT 3
Q9D8B7 PRELIMINARY; PRT; 310 AA.
AC Q9D8B7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;

```

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havaehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

Query Match 49.0%; Score 152; DB 11; Length 310;
Best Local Similarity 99.6%; Pred. No. 1.9e-155;
Matches 252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 SQTSDPRIEMKKIQDQTTVYVFNKIQGLAGRTDVPFKTSRLRWVTRSDSAIYRCEV 117
DB 58 SQTSDPRIEMKKIQDQTTVYVFNKIQGLAGRTDVPFKTSRLRWVTRSDSAIYRCEV 117

QY 118 VALNDRKEVDEITIELIVQKVPVPCRIAPAVPVGKTATLQCSSEGYPHYNRYND 177
DB 118 VALNDRKEVDEITIELIVQKVPVPCRIAPAVPVGKTATLQCSSEGYPHYNRYND 177

QY 178 VPLPTDSRANPQNSSFHNVSETGLVFNHKKDSGGYCYCIASNDAGAACRCQDMEV 237
DB 178 VPLPTDSRANPQNSSFHNVSETGLVFNHKKDSGGYCYCIASNDAGAACRCQDMEV 237

QY 238 YDLNLAGIIGGVLLVILAVITMGICCAAYRGCFISSKQDGSYKSPGKHGVDVNYRTS 297
DB 238 YDLNLAGIIGGVLLVILAVITMGICCAAYRGCFISSKQDGSYKSPGKHGVDVNYRTS 297

QY 298 BEGDFPRHKSFFVI 310
DB 298 BEGDFPRHKSFFVI 310

RESULT 4
Q8BT59 PRELIMINARY; PRT; 64 AA.
AC Q8BT59;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Junction cell adhesion molecule 3 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK017692; BAC25526.1; -.
FT NON_TER 1
SQ SEQUENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;

Query Match 20.6%; Score 64; DB 11; Length 64;
Best Local Similarity 100.0%; Pred. No. 7.3e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 GGVLLVILAVITMGICCAAYRGCFISSKQDGSYKSPGKHGVDVNYRTSBEGRPHKS 306
DB 1 GGVLLVILAVITMGICCAAYRGCFISSKQDGSYKSPGKHGVDVNYRTSBEGRPHKS 60

QY 307 SPVI 310
DB 61 SPVI 64

RESULT 5
Q96FL1 PRELIMINARY; PRT; 309 AA.
AC Q96FL1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010690; AAH10690.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;

Query Match 7.7%; Score 24; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.8e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 PRPHYSWYRNDVPLPTDSRANPRF 190
DB 166 PRPHYSWYRNDVPLPTDSRANPRF 189

RESULT 6
Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein FLJ90828).
DE FLJ90828) (Hypothetical protein FLJ90828).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

```

RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Aurand-lions M.A., Johnson-leger C., Wong C., Dupasquier L.;
RT "Heterogeneity of endothelial junctions is reflected by differential
RT expression and specific subcellular localization of the three JAM
RT family members.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Aurand-lions M.A., Johnson-leger C., Iamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial
RT junctions.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sachs U.J.H., Sva O., Berghoefer H., Santoso S.;
RT "Characterization of Junctional Adhesion Molecule-3 on Human
RT Platelets: A New Member of Immunoglobulin Superfamily.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Maehiro Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA EMBL; AF356518; AAK27221.1; -
DR EMBL; AF344431; CAC69845.1; -
DR EMBL; AF448478; AAM20925.1; -
DR EMBL; AK074769; BAC11195.1; -
DR EMBL; AK075309; BAC11538.1; -
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein; Signal.
FT SIGNAL 1 30 POTENTIAL.
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EA1DAB9 CRC64;

Query Match 7.7%; Score 24; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.9e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
Db 167 PRPHYSWYRNDVPLPTDSRANPRF 190

RESULT 7
Q8WNL8 PRELIMINARY; PRT; 355 AA.
ID Q8WNL8
AC Q8WNL8
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction adhesion molecule 3.
GN JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hearn T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Phillips H.M.;
RT "Narrowing the critical region within 11q24-qter for hypoplastic left

RT heart and identification of a candidate gene, JAM3, expressed during
RT cardiogenesis.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA EMBL; AJ416101; CAC94776.1; -
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain.
FT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.
SQ SEQUENCE 355 AA; 39602 MW; 981577DEA7B1D4F8 CRC64;

Query Match 7.7%; Score 24; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
Db 212 PRPHYSWYRNDVPLPTDSRANPRF 235

RESULT 8
Q8RQG2 PRELIMINARY; PRT; 92 AA.
ID Q8RQG2
AC Q8RQG2
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable NAD(P)H-flavin oxidoreductase (fragment).
GN CMK16.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=rim-rol;
RA Nishizawa M., Itoi Y., Ito S., Inoue M.;
RT "Genes induced by glycine in Bacillus cereus.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
DR EMBL; AB083554; BAB88982.1; -
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000415; Nitroreductase.
DR Pfam; PF00881; Nitroreductase; 1.
FT NON_TER 1 1
SQ SEQUENCE 92 AA; 10168 MW; E9C9B25BAF89B39 CRC64;

Query Match 2.6%; Score 8; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 RKEVDEIT 130
Db 81 RKEVDEIT 89

RESULT 9
Q818S1 PRELIMINARY; PRT; 131 AA.
ID Q818S1
AC Q818S1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Odorant-binding protein G.38B.a.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu P., Smith D.P.;

"Identification of distinct families of odorant-binding in the genome of Anopheles gambiae." to the EMBL/GenBank/DBJ databases.

Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 EMBL: AY146730; AAO12090.1; --
 DR GO: GO:0005549; P: odorant binding; IEA.
 DR GO: GO:0006810; P: transport; IEA.
 DR InterPro: IPR006170; P: PBP_GOBP.
 DR Pfam: PF01395; P: PBP_GOBP.1.
 SQ SEQUENCE 131 AA; 14884 MW; FCTD52E9740E2A64 CRC64;

Query Match 2.6%; Score 8; DB 5; Length 131;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 IGGVLWVL 253
 |||||
 Db 7 IGGVLWVL 14

RESULT 10

Q8AZH5 PRELIMINARY; PRT; 165 AA.
 AC Q8AZH5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Capsid protein (Fragment).
 GN VP60.
 OS Rabbit hemorrhagic disease virus (RHDV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Lagovirus.
 OX NCBI_TaxID=11976;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=94-02;
 RX MEDLINE=2242426; PubMed=12536296;
 RA Le Gall-Recule G., Zwingelstein F., Laurent S., de Boisseson C.,
 Portejoie Y., Raschaert D.;
 RT "Phylogenetic analysis of rabbit hemorrhagic disease virus in France between 1993 and 2000, and the characterisation of RHDV antigenic variants."
 RL Arch. Virol. 148:65-81(2003).
 DR EMBL: AJ535102; CAD59257.1; --
 DR InterPro: IPR004005; Calici_coat.
 DR Pfam: PF00915; Calici_coat; 1.
 FT NON_TER 1
 FT NON_TER 165
 SQ SEQUENCE 165 AA; 16991 MW; 9A6B06A848F6BD8 CRC64;

Query Match 2.6%; Score 8; DB 12; Length 165;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 PAAVPVGK 154
 |||||
 Db 54 PAAVPVGK 61

RESULT 11

Q99U70 PRELIMINARY; PRT; 204 AA.
 AC Q99U70;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Conserved hypothetical protein (Hypothetical protein SAV1417).
 GN SAV1417 OR SA1250.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879;
 RN [1]
 RP SEQUENCE FROM N.A.

Query Match 2.6%; Score 8; DB 16; Length 204;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IAGIIGGV 249
 |||||
 Db 181 IAGIIGGV 188

RESULT 13

Q8CSL1 PRELIMINARY; PRT; 204 AA.
 ID Q8CSL1
 AC Q8CSL1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)

SPECIES=S. aureus (strain Mu50), and S. aureus (strain N315);
 MEDLINE=21311952; PubMed=11418146;
 RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanchisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003362; BAB57579.1; --
 DR EMBL: AP003133; BAB42510.1; --
 DR PIR: A89919; A89919.
 DR InterPro: IPR008934; AcPase_VanParase.
 DR InterPro: IPR000326; PA_PTPase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidPPc; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 204 AA; 22685 MW; 009CF65D8B1PBDP2 CRC64;

Query Match 2.6%; Score 8; DB 16; Length 204;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IAGIIGGV 249
 |||||
 Db 181 IAGIIGGV 188

RESULT 12

Q8NWR5 PRELIMINARY; PRT; 204 AA.
 AC Q8NWR5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Conserved hypothetical protein.
 GN MW1306.
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 DR EMBL: AF004826; BAB95171.1; --
 DR InterPro: IPR008934; AcPase_VanParase.
 DR InterPro: IPR000326; PA_PTPase.
 DR Pfam: PF01569; PAP2; 1.
 KW Complete proteome.
 SQ SEQUENCE 204 AA; 22715 MW; 0CFDFB30FB03C497 CRC64;

Query Match 2.6%; Score 8; DB 16; Length 204;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IAGIIGGV 249
 |||||
 Db 181 IAGIIGGV 188

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GN Conserved hypothetical protein.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
  Chen Y., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016747; AA004706.1; -.
DR InterPro; IPR008934; AcPase_VanPerase.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPPc; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 204 AA; 22838 MW; CC6635270009F674 CRC64;

Query Match 2.6%; Score 8; DB 16; Length 204;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 IAGIIGGV 249
Db 181 IAGIIGGV 188
|||||

RESULT 14
P95439 PRELIMINARY; PRT; 206 AA.
AC P95439;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE PSCK.
GN PSCK.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=388;
RX MEDLINE=97126825; PubMed=8971719;
RA Yahr T.L., Goranson J., Frank D.W.;
RT "Exoenzyme S of Pseudomonas aeruginosa is secreted by a type III
  pathway.";
RL Mol. Microbiol. 22:991-1003(1996).
DR EMBL; U56077; AAC44782.1; -.
SQ SEQUENCE 206 AA; 23971 MW; 8DD0E751E26BDF88 CRC64;

Query Match 2.6%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRRLRLRL 11
Db 160 SRRLRLRL 167
|||||

RESULT 15
Q91313 PRELIMINARY; PRT; 208 AA.
AC Q91313;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type III export protein PscK.
GN PSCK OR PA1724.
OS Pseudomonas aeruginosa.

```

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
  Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
  Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
  Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
  Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
  Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
  opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AB004598; AAG05113.1; -.
DR PIR; D83431; D83431.
KW Complete proteome.
SQ SEQUENCE 208 AA; 23898 MW; 74F6B5848FE9E5B8 CRC64;

Query Match 2.6%; Score 8; DB 16; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRRLRLRL 11
Db 160 SRRLRLRL 167
|||||

Search completed: June 15, 2004, 11:11:55
Job time : 37 secs

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 10:50:54 ; Search time 51.5 Seconds
(without alignments)
1700.771 Million cell updates/sec

Title: US-09-524-531c-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLARLPHFL.....VNYIRTSRGDFRHKSSFVI 310

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1633	100.0	310	3 AAB27278	Aab27278 Murine co
2	1633	100.0	310	3 AAB27272	Aab27272 Human con
3	1409	86.3	310	3 -AAY96735	Aay96735 PRO1868,
4	1409	86.3	310	3 AAB33457	Aab33457 Human PRO
5	1409	86.3	310	3 AAB27276	Aab27276 Human con
6	1409	86.3	310	4 AAB80272	Aab80272 Human PRO
7	1409	86.3	310	4 AAB93905	Aam93905 Human pol
8	1409	86.3	310	4 AAM93323	Aam93323 Human pol
9	1409	86.3	310	4 AAU12440	Aau12440 Human PRO
10	1409	86.3	310	4 AAB80383	Aab80383 Secreted
11	1409	86.3	310	4 AAB80408	Aab80408 Secreted
12	1409	86.3	310	4 AAB80409	Aab80409 Secreted
13	1409	86.3	310	5 ABG92709	Abg92709 Human sec
14	1409	86.3	310	5 ABG91361	Abg91361 Novel hum
15	1409	86.3	310	5 ABB84947	Abb84947 Human PRO
16	1409	86.3	310	5 ABG65297	Abg65297 Human alb
17	1409	86.3	310	5 ABG65296	Abg65296 Human alb
18	1409	86.3	310	5 ABG65298	Abg65298 Human alb
19	1409	86.3	310	5 ABG31401	Abg31401 Human PRO
20	1409	86.3	310	5 ABB95553	Abb95553 Human ang
21	1409	86.3	310	6 ABU71650	Abu71650 Human PRO
22	1409	86.3	310	6 ABU72377	Abu72377 Novel hum
23	1409	86.3	310	6 ABU80867	Abu80867 Human sec
24	1409	86.3	310	6 ABO17884	Abol17884 Novel hum
25	1409	86.3	310	6 ABU71505	Abu71505 Human PRO

26	1409	86.3	310	6 ADA57610	Ada57610 Human sec
27	1409	86.3	310	6 ADA57611	Ada57611 Human sec
28	1409	86.3	310	6 ADA57309	Ada57309 Human sec
29	1409	86.3	310	6 ABP71277	Abp71277 Human Jun
30	1409	86.3	310	6 ABU81138	Abu81138 Human PRO
31	1409	86.3	310	6 ABU71951	Abu71951 Human sec
32	1409	86.3	310	6 ABO01834	Abo01834 Novel hum
33	1409	86.3	310	6 ABU66838	Abu66838 Human PRO
34	1409	86.3	310	6 ABUS4407	AbuS4407 Human sec
35	1409	86.3	310	6 ABO47422	Abo47422 Human sec
36	1409	86.3	310	6 ABG73314	Abg73314 Human PRO
37	1409	86.3	310	6 ABUS9919	AbuS9919 Novel sec
38	1409	86.3	310	6 ABO25109	Abo25109 Human sec
39	1409	86.3	310	6 ABUS4559	Abu64559 Human sec
40	1409	86.3	310	6 ABUS7405	Abu67405 Human sec
41	1409	86.3	310	6 ABO14925	Abo14925 Human sec
42	1409	86.3	310	6 ABUS0813	Abu60813 Human sec
43	1409	86.3	310	6 ABUS7114	Abu67114 Human PRO
44	1409	86.3	310	6 ABUS1236	Abu81236 Human PRO
45	1409	86.3	310	6 ABUS6982	Abu69682 Novel hum

ALIGNMENTS

RESULT 1
AAB27278
ID AAB27278 standard; protein; 310 AA.
XX
AC AAB27278;
XX
DT 23-FEB-2001 (first entry)
XX
DB Murine confluency regulated adhesion molecule 1.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; mouse;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Mus sp.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMP DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI: 2000-587436/55.
XX
N-PSDB; AAA97189.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
CRAM-2) polypeptide, useful for treatment of tumors, inflammation
reactions and modulating vascular permeability.
XX
PS Example; Fig 8; 59pp; English.
XX
CC The present sequence is the murine confluency regulated adhesion molecule
1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 1633; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-122;

XX WO200036102-A2.
XX 22-JUN-2000.
XX PF 01-DEC-1999; 99WO-US028634.
XX PR 16-DEC-1998; 98US-0112851P.
XX PR 16-DEC-1998; 98US-0113145P.
XX PR 22-DEC-1998; 98US-0113511P.
XX PR 12-JAN-1999; 99US-0115558P.
XX PR 12-JAN-1999; 99US-0115733P.
XX PR 09-FEB-1999; 99US-0119341P.
XX PR 10-FEB-1999; 99US-0119537P.
XX PR 12-FEB-1999; 99US-0119565P.
XX PR 02-JUN-1999; 99WO-US012252.
XX (GETH) GENENTECH INC.
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX WPI; 2000-431586/37.
XX N-PSDB; AAA51285.
XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a
XX transmembrane polypeptide.
XX Claim 1; Fig 14; 154pp; English.
XX This is PRO1869, a putative homologue of A33 antigen, a known colorectal
XX cancer-associated marker. The invention concerns novel secreted and
XX transmembrane proteins, designated PRO polypeptides. The cDNA and gene
XX sequences are useful in the recombinant production of PRO polypeptides,
XX as a hybridization probe to screen libraries to isolate cDNAs with
XX sequence identity to PRO polypeptides or to map the gene encoding the PRO
XX polypeptides and analyzing genetic disorders. The cDNA/gene can also be
XX used to produce transgenic animals useful for the development and
XX screening of therapeutically useful reagents. They can also be used in
XX gene therapy, e.g. to replace a defective gene
XX Sequence 310 AA;
Query Match 86.3%; Score 1409; DB 3; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
QY 1 MALSRRLRLRLYLARLPHFLLLLFRGCMTEAVNLKSNRNFPVHHFESVELSCIITHSQ 60
Db 1 MALRRPRLRLCARLPDFLLLLFRGLIGAVNLKSNRTPVQVBFESVELSCIITHSQ 60
QY 61 SDPRIEMKKIQDQTTVVYFDNKKIQDLAGRTDVFGKTSIRIWNVTRSDSAIYRCEVVAL 120
Db 61 SDPRIEMKKIQDQTTVVYFDNKKIQDLAGRTDVFGKTSIRIWNVTRSDSAIYRCEVVAR 120
QY 121 NDRKEVDEITIELIVQKPTPVCRIPAAVPVCKTATLQCESEGEPRPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQKPTPVCRIPAAVPVCKMATLHCQSEGEPRPHYSWYRNDVPL 180
QY 181 PTDSTRANPRQNSFHVNSGTGLVFNVAHKDQSGQYICASNDAGARCEGQDMEVYDL 240
Db 181 PTDSTRANPRNSFHLNSETGLVPTVAHKDQSGQYICASNDAGSARCEQEMEYDL 240
QY 241 NIAGIIGGVLVILVLAITMGICCAIRRCFTISSKQDGEYSKPKKHGQVNYIRISEG 300
Db 241 NIGGIIGGVLVILVLAITLIGICCAIRRGYFINNKQDGEYSKPKGPGVNYIRITDEG 300
QY 301 DFRHKSFEVI 310
Db 301 DFRHKSFEVI 310

RESULT 4
AAB33457
ID AAB33457 standard; protein; 310 AA.
XX AC AAB33457;
XX 29-JAN-2001 (first entry)
XX Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
XX dermatologic; antiarthritic; antirheumatic; immunosuppressive;
XX haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
XX antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
XX osteoarthritis; spondyloarthropathy; systemic sclerosis; rheumatoid arthritis;
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
XX autoimmune thrombocytopenia; immune-mediated renal disease;
XX demyelinating disease; hepatobiliary disease; Whipple's disease;
XX inflammatory bowel disease; gluten-sensitive enteropathy;
XX autoimmune disease; immune-mediated skin disease; allergic disease;
XX immunological disease; transplantation associated disease;
XX graft rejection; graft-versus-host-disease.
XX Homo sapiens.
XX WO200053758-A2.
XX 14-SEP-2000.
XX 02-MAR-2000; 2000WO-US005841.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
XX 12-MAR-1999; 99US-0123957P.
XX 12-MAR-1999; 99US-0125775P.
XX 12-APR-1999; 99US-0128849P.
XX 20-APR-1999; 99WO-US008615.
XX 28-APR-1999; 99US-0131445P.
XX 04-MAY-1999; 99US-0132371P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-OCT-1999; 99US-0162506P.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.

XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

XX PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX DR WPI; 2000-572271/53.

XX DR N-PSDB; AAC58622.

XX PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of

XX PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

XX PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX PS Claim 33; Fig 88; 309pp; English.

XX CC The present invention describes sixty four human PRO proteins which can

XX CC be used in the treatment of immune related diseases. The human PRO

XX CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

XX CC treating and diagnosing immune related disorders. The disorders are

XX CC selected from systemic lupus erythematosus, rheumatoid arthritis,

XX CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

XX CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

XX CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

XX CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

XX CC immune-mediated renal disease, demyelinating diseases of the central and

XX CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel

XX CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune

XX CC or immune-mediated skin diseases, allergic diseases, immunological

XX CC diseases of the lung, and transplantation associated diseases including

XX CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578

XX CC represent PCR primers and hybridisation probes used in the isolation of

XX CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477

XX CC represent human PRO polynucleotide and protein sequences given in the

XX CC exemplification of the present invention

XX SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 3; Length 310;

Best Local Similarity 85.8%; Pred. No. 1.1e-104;

Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLPHFLLPRGCMIEAVNLKSSNRNPVWHEFESVELSCIITHSQ 60

Db 1 MALRRPRLRLCARLPDFLLPRGCLIGAVNLKSSNRTPVWQEFSSVELSCIITHSQ 60

Qy 61 SDPRIWKIKQDQTTVYVFNKIQGLAGRTDVGKTSLRIMNVTRSDSALYRCVVAL 120

Db 61 SDPRIWKIKQDQTTVYVFNKIQGLAGRTDVGKTSLRIMNVTRSDSALYRCVVAL 120

Qy 121 NDRKEVDRIITELIVQKVPVPCRIIPAAVPVGTATLQOESGEGYPRPHYSWTRNDVPL 180

Db 121 NDRKEIDEIVIELTVQKVPVPCRPVAVPVGMATLHCQESGEGYPRPHYSWTRNDVPL 180

Qy 181 PTDGRANPRFNSFHLNSETGLVFAVHKDDSGQYVCIASNDAGAACRCQDMVYDL 240

Db 181 PTDGRANPRFNSFHLNSETGLVFAVHKDDSGQYVCIASNDAGAACRCQDMVYDL 240

Qy 241 NIAGIIGVLVLLVLAIVTMGICCAVRRGCFISSKQGESYKSPGKHGDNVYIRTSBEG 300

Db 241 NIGGIIGVLVLLVLAIVTMGICCAVRRGCFISSKQGESYKSPGKHGDNVYIRTSBEG 300

Qy 301 DFRHKSFSVI 310

Db 301 DFRHKSFSVI 310

RESULT 5

AAB27276

ID AAB27276 standard; protein; 310 AA.

XX AC AAB27276;

XX XX

DT 23-FEB-2001 (first entry)

XX Human confluency regulated adhesion molecule 1 #2.

XX Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;

XX inflammation; cancer; wound; angiogenesis; human;

XX confluency regulated adhesion molecule 1; CRAM-1; JAM-2.

XX OS Homo sapiens.

XX WO200053749-A2.

XX PD 14-SBP-2000.

XX PF 13-MAR-2000; 2000WO-EP002219.

XX PR 11-MAR-1999; 99EP-00200746.

XX PA (RMFD-) RMP DICTAGENE SA.

XX PI Imhof BA, Aurrand-Lions M;

XX DR WPI; 2000-587436/55.

XX DR N-PSDB; AAA95306.

XX PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or

XX PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation

XX PT reactions and modulating vascular permeability.

XX PS Claim 2; Fig 6; 59pp; English.

XX CC The present sequence is the human confluency regulated adhesion molecule

XX CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion

XX CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein

XX CC and coding sequence can be used in the treatment of cancer, inflammation,

XX CC to modulate cell-cell interactions and angiogenesis, and in the

XX CC modulation of wound healing

XX SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 3; Length 310;

Best Local Similarity 85.8%; Pred. No. 1.1e-104;

Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLPHFLLPRGCMIEAVNLKSSNRNPVWHEFESVELSCIITHSQ 60

Db 1 MALRRPRLRLCARLPDFLLPRGCLIGAVNLKSSNRTPVWQEFSSVELSCIITHSQ 60

Qy 61 SDPRIWKIKQDQTTVYVFNKIQGLAGRTDVGKTSLRIMNVTRSDSALYRCVVAL 120

Db 61 SDPRIWKIKQDQTTVYVFNKIQGLAGRTDVGKTSLRIMNVTRSDSALYRCVVAL 120

Qy 121 NDRKEVDRIITELIVQKVPVPCRIIPAAVPVGTATLQOESGEGYPRPHYSWTRNDVPL 180

Db 121 NDRKEIDEIVIELTVQKVPVPCRPVAVPVGMATLHCQESGEGYPRPHYSWTRNDVPL 180

Qy 181 PTDGRANPRFNSFHLNSETGLVFAVHKDDSGQYVCIASNDAGAACRCQDMVYDL 240

Db 181 PTDGRANPRFNSFHLNSETGLVFAVHKDDSGQYVCIASNDAGAACRCQDMVYDL 240

Qy 241 NIAGIIGVLVLLVLAIVTMGICCAVRRGCFISSKQGESYKSPGKHGDNVYIRTSBEG 300

Db 241 NIGGIIGVLVLLVLAIVTMGICCAVRRGCFISSKQGESYKSPGKHGDNVYIRTSBEG 300

Qy 301 DFRHKSFSVI 310

Db 301 DFRHKSFSVI 310

RESULT 6

AAB80272

ID AAB80272 standard; protein; 310 AA.

XX AC AAB80272;

XX XX

CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRRLRLRLYLARLPHFFLLFRGCMIBAVNLKSSNRNPVHVFESVLSLCIITHSQ 60
DB 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFESVLSLCIITHSQ 60

QY 61 SDPRIWKKI QDQTTVYVFDNKIQGLAGRTDVFQKTSLRIMNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIWKKI QDQTTVYVFDNKIQGLAGRTDVFQKTSLRIMNVTRSDSAIYRCEVVAL 120

QY 121 NDRKEVDEITIELVQKPTVPCRIIPAAVPGVGTATLQOESGSGYRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQKPTVPCRVKPAVPGVGTATLQOESGSGYRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFNSGSHVNSSETGLVFNVAHKDDSGQYCIASNDAGAACRCEQMEVYDL 240
DB 181 PTDSRANPRFNSGSHVNSSETGLVFNVAHKDDSGQYCIASNDAGAACRCEQMEVYDL 240

QY 241 NIAGIIGGLVWLVLAVITWGIICCAVRRGCFISSKQDGSYKSPGKHGDNVYIRTSBEG 300
DB 241 NIAGIIGGLVWLVLAVITWGIICCAVRRGCFISSKQDGSYKSPGKHGDNVYIRTSBEG 300

QY 301 DFRHKSFPVI 310
DB 301 DFRHKSFPVI 310

RESULT 8
AAW93323 standard; protein; 310 AA.
XX
AC AAW93323;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 2845.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
FN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
XX
PR 11-JAN-2000; 2000JP-00118774.
XX
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI: 2001-524255/58.
XX
DR N-PSDB: AAK94243.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRRLRLRLYLARLPHFFLLFRGCMIBAVNLKSSNRNPVHVFESVLSLCIITHSQ 60
DB 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFESVLSLCIITHSQ 60

QY 61 SDPRIWKKI QDQTTVYVFDNKIQGLAGRTDVFQKTSLRIMNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIWKKI QDQTTVYVFDNKIQGLAGRTDVFQKTSLRIMNVTRSDSAIYRCEVVAL 120

QY 121 NDRKEVDEITIELVQKPTVPCRIIPAAVPGVGTATLQOESGSGYRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQKPTVPCRVKPAVPGVGTATLQOESGSGYRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFNSGSHVNSSETGLVFNVAHKDDSGQYCIASNDAGAACRCEQMEVYDL 240
DB 181 PTDSRANPRFNSGSHVNSSETGLVFNVAHKDDSGQYCIASNDAGAACRCEQMEVYDL 240

QY 241 NIAGIIGGLVWLVLAVITWGIICCAVRRGCFISSKQDGSYKSPGKHGDNVYIRTSBEG 300
DB 241 NIAGIIGGLVWLVLAVITWGIICCAVRRGCFISSKQDGSYKSPGKHGDNVYIRTSBEG 300

QY 301 DFRHKSFPVI 310
DB 301 DFRHKSFPVI 310

RESULT 9
AAU12440
ID AAU12440 standard; protein; 310 AA.
XX
AC AAU12440;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1868 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
XX
PR 01-DEC-1999; 99WO-US028634.
XX
PR 02-DEC-1999; 99WO-US028551.
XX
PR 02-DEC-1999; 99WO-US028564.
XX
PR 09-DEC-1999; 99US-0170262P.
XX
PR 16-DEC-1999; 99WO-US030095.

XX
SQ Sequence 310 AA;
Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRRLRLYLRLPFFLLFRGCMIEAVNLKSSNRNPVVFHESVELSCIITHSQT 60
DB 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVOEFESVELSCIITHSQT 60

QY 61 SDPRIWKIKDQGTTFVFDNKIQGLAGRTDVFQKTSLRINWVTRSDSALYRCEVVAL 120
DB 61 SDPRIWKIKDQGTTFVFDNKIQGLAGRTDVFQKTSLRINWVTRSDSALYRCEVVAL 120

QY 121 NDRKEVDITIELIVQKPTVPCRIIPAAVPGVGTATLQCOSEGYPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQKPTVPCRVKPAVPGVGTATLQCOSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFQNSFHVNSSETGLVFNVAHKDQSGQYCIASNDAGARCEQDMEVYDL 240
DB 181 PTDSRANPRFQNSFHVNSSETGLVFNVAHKDQSGQYCIASNDAGARCEQDMEVYDL 240

QY 241 NIAGIIGGLVVLAVLAVITMGICCAVRRGCTISSKODGESYKSPGKHGDNVYIRTSEEG 300
DB 241 NIAGIIGGLVVLAVLAVITMGICCAVRRGCTISSKODGESYKSPGKHGDNVYIRTSEEG 300

QY 301 DFRHKSFSVI 310
DB 301 DFRHKSFSVI 310

RESULT 11
AAB80408
ID AAB80408 standard; protein; 310 AA.
AC AAB80408;
XX
XX
XX 24-APR-2001 (first entry)
XX
XX Secreted protein encoded by gene #38.
XX
XX Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
XX cerebrovascular; infection; food.
XX
XX Homo sapiens.
XX
XX WO200107459-A1.
XX
XX 01-FEB-2001.
XX
XX 20-JUL-2000; 2000WO-US019735.
XX
XX 23-JUL-1999; 99US-0145220P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
XX Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX WPI; 2001-123261/13.
XX
XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
XX preventing and treating e.g. autoimmune, hyperproliferative,
XX cardiovascular, and ocular diseases or disorders and microorganism
XX infections.
XX
XX Claim 11; Page 557-558; 601pp; English.
XX
XX The present invention relates to 29 human secreted proteins. The
XX invention is used to prevent autoimmune diseases e.g. rheumatoid
XX arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
XX liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular

CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;
Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRRLRLYLRLPFFLLFRGCMIEAVNLKSSNRNPVVFHESVELSCIITHSQT 60
DB 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVOEFESVELSCIITHSQT 60

QY 61 SDPRIWKIKDQGTTFVFDNKIQGLAGRTDVFQKTSLRINWVTRSDSALYRCEVVAL 120
DB 61 SDPRIWKIKDQGTTFVFDNKIQGLAGRTDVFQKTSLRINWVTRSDSALYRCEVVAL 120

QY 121 NDRKEVDITIELIVQKPTVPCRIIPAAVPGVGTATLQCOSEGYPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQKPTVPCRVKPAVPGVGTATLQCOSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFQNSFHVNSSETGLVFNVAHKDQSGQYCIASNDAGARCEQDMEVYDL 240
DB 181 PTDSRANPRFQNSFHVNSSETGLVFNVAHKDQSGQYCIASNDAGARCEQDMEVYDL 240

QY 241 NIAGIIGGLVVLAVLAVITMGICCAVRRGCTISSKODGESYKSPGKHGDNVYIRTSEEG 300
DB 241 NIAGIIGGLVVLAVLAVITMGICCAVRRGCTISSKODGESYKSPGKHGDNVYIRTSEEG 300

QY 301 DFRHKSFSVI 310
DB 301 DFRHKSFSVI 310

RESULT 12
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
XX
XX
XX
XX 24-APR-2001 (first entry)
XX
XX Secreted protein encoded by gene #39.
XX
XX Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
XX cerebrovascular; infection; food.
XX
XX Homo sapiens.
XX
XX WO200107459-A1.
XX
XX 01-FEB-2001.
XX
XX 20-JUL-2000; 2000WO-US019735.
XX
XX 23-JUL-1999; 99US-0145220P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
XX Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX WPI; 2001-123261/13.
XX
XX New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
XX preventing and treating e.g. autoimmune, hyperproliferative,
XX cardiovascular, and ocular diseases or disorders and microorganism
XX infections.
XX
XX Claim 11; Page 559-560; 601pp; English.

CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRLRLRLYLPHFPFLLLFRGCMTEAVNLKSSNRNPVVFESVELSCIITHSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLLFRGLLGAVNLKSSNRNPVVFESVELSCIITDSQT 60

QY 61 SDPRIEMKKIQDQTTTYYVFDNKIQDLAGRTDVGKTSILRIWNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIEMKKIQDQTTTYYVFDNKIQDLAGRAEILGKTSILRIWNVTRSDSAIYRCEVVAR 120

QY 121 NDRKEVDEITIELIVQVKPVTVCRIIPAAVPVGTATLQCESEGVPRPHYSWRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPVTVCRIIPAAVPVGTATLQCESEGVPRPHYSWRNDVPL 180

QY 181 PTDSRANPRFQNSPHVNSSETGLTFVNAVHKDDSGQYCIASNDAGAACRCEQDMEVYDL 240
DB 181 PTDSRANPRFQNSPHVNSSETGLTFVNAVHKDDSGQYCIASNDAGAACRCEQDMEVYDL 240

QY 241 NTAGIIGGVLLVILVAVTMGICCAVRCGCTPISKQDGSYKSPKHDGVNYRTSBE 300
DB 241 NTAGIIGGVLLVILVAVTMGICCAVRCGCTPISKQDGSYKSPKHDGVNYRTSBE 300

QY 301 DPHKSSFVI 310
DB 301 DPHKSSFVI 310

RESULT 13
ABG92709
ID ABG92709 standard; protein; 310 AA.
AC ABG92709;
DT 18-NOV-2002 (first entry)
DE Human secreted protein PRO1868.
XX
KW Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
KW PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW inflammatory disorder; immune related disease; rheumatoid arthritis;
KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW psoriasis; allergic disease of the lung; graft-versus host disease;
KW tumour; gene therapy.
XX
OS Homo sapiens.
XX
FN US2002098506-A1.
XX
PD 25-JUL-2002.
XX
PF 27-DEC-2001; 2001US-00033301.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 22-DEC-1998; 98US-0113145P.
PR 12-JAN-1999; 98US-0113511P.
PR 12-JAN-1999; 98US-0115558P.
PR 12-JAN-1999; 98US-0115565P.
PR 12-JAN-1999; 98US-0115733P.

PR 09-FEB-1999; 99US-0119341P.
PR 12-FEB-1999; 99US-0119337P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX (GETH) GENENTECH INC.
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX WPI; 2002-690475/74.
XX N-PSDB; ABS68392.
XX Novel secreted and transmembrane polypeptides and polynucleotides useful
XX for diagnosis and treatment of inflammatory disorders and immune-related
XX diseases, and identifying modulators.
XX Claim 12; Fig 14; 125pp; English.
XX The invention relates to an isolated polypeptide having at least 80%
XX amino acid sequence identity to secreted and transmembrane polypeptides
XX PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
XX PRO1927 and their encoding nucleic acids. Also included are vectors, host
XX cells and antibodies against PRO polypeptides. PRO proteins are useful
XX for identifying modulators of the polypeptide. PRO1868 useful for the
XX diagnosis and treatment of inflammatory and immune related diseases
XX including systemic lupus erythematosus, rheumatoid arthritis, systemic
XX sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
XX infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
XX versus host disease and tumours. PRO nucleic acids are useful for
XX constructing hybridisation probes for mapping the gene that encodes that
XX PRO and for the genetic analysis of individuals with genetic disorders,
XX and for generating transgenic animals which are useful in the development
XX and screening of therapeutically useful reagents. PRO nucleic acids are
XX also useful for gene therapy, chromosome identification, and tissue
XX typing. PRO proteins are useful as molecular weight markers for protein
XX electrophoresis purposes. The anti-PRO antibodies are useful in
XX diagnostic assays for PRO, e.g. detecting its expression in specific
XX cells, tissues or serum and for affinity purification of PRO. The present
XX sequence represents a PRO protein
XX
SQ Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 5; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRLRLRLYLPHFPFLLLFRGCMTEAVNLKSSNRNPVVFESVELSCIITHSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLLFRGLLGAVNLKSSNRNPVVFESVELSCIITDSQT 60

QY 61 SDPRIEMKKIQDQTTTYYVFDNKIQDLAGRTDVGKTSILRIWNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIEMKKIQDQTTTYYVFDNKIQDLAGRAEILGKTSILRIWNVTRSDSAIYRCEVVAR 120

QY 121 NDRKEVDEITIELIVQVKPVTVCRIIPAAVPVGTATLQCESEGVPRPHYSWRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPVTVCRIIPAAVPVGTATLQCESEGVPRPHYSWRNDVPL 180

QY 181 PTDSRANPRFNSFFVNSVETGLVFNVAHKDSDGQYICIASNDAGAACRCEQDMEVYDL 240
 DB 181 PTDSRANPRFNSFFVNSVETGLVFNVAHKDSDGQYICIASNDAGAACRCEQDMEVYDL 240
 QY 241 NIAGIIGGVLLVILAVITWIGICCAVRRCFISKQDGSYKSPGKHGCVNVRTSEEG 300
 DB 241 NIAGIIGGVLLVILAVITWIGICCAVRRCFISKQDGSYKSPGKHGCVNVRTSEEG 300
 QY 301 DFRHKSFSVI 310
 DB 301 DFRHKSFSVI 310

RESULT 14
 ABG91361
 ID ABG91361 standard; protein; 310 AA.
 XX AC ABG91361;
 XX DT 29-NOV-2002 (first entry)
 XX DE Novel human secreted protein #7.
 XX KW Human; secreted protein; transmembrane protein; gene mapping; transgenic;
 XX OS immunogenic.
 XX OS Homo sapiens.
 XX PN US2002098505-A1.
 XX PD 25-JUL-2002.
 XX PF 28-DEC-2001; 2001US-00033246.
 XX PR 04-AUG-1998; 98US-0095325P.
 XX PR 16-DEC-1998; 98US-0112851P.
 XX PR 16-DEC-1998; 98US-0113145P.
 XX PR 22-DEC-1998; 98US-0113511P.
 XX PR 12-JAN-1999; 99US-0115558P.
 XX PR 12-JAN-1999; 99US-0115565P.
 XX PR 09-FEB-1999; 99US-0119341P.
 XX PR 10-FEB-1999; 99US-0119537P.
 XX PR 12-FEB-1999; 99US-0119965P.
 XX PR 29-JUN-1999; 99WO-US012252.
 XX PR 29-OCT-1999; 99US-0162506P.
 XX PR 01-DEC-1999; 99WO-US028634.
 XX PR 02-DEC-1999; 99WO-US028551.
 XX PR 09-DEC-1999; 99US-0170282P.
 XX PR 11-FEB-2000; 2000WO-US003565.
 XX PR 22-FEB-2000; 2000WO-US004414.
 XX PR 02-MAR-2000; 2000WO-US005841.
 XX PR 03-MAR-2000; 2000US-0187202P.
 XX PR 30-MAR-2000; 2000WO-US008439.
 XX PR 30-MAY-2000; 2000WO-US014941.
 XX PR 02-JUN-2000; 2000WO-US015264.
 XX PR 01-DEC-2000; 2000WO-US032678.
 XX PR 25-MAY-2001; 2001US-00866034.
 XX PA (GETH) GENENTECH INC.
 XX PI Botstein D, Desnoyers L, Ferrara N, Pong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK,
 PI Wood WI;
 XX WPI; 2002-665999/71.
 XX DR N-PSDB; ABS67460.
 XX PT New human secreted and transmembrane (PRO) polypeptides, useful for
 PT treating conditions requiring PRO polypeptides, for screening PRO
 PT antagonists and agonists useful as drug candidates.
 XX PS Claim 12; Fig 14; 125pp; English.

XX CC The invention relates to new human secreted and transmembrane proteins
 CC (PRO) and nucleic acids of the invention. The polypeptides can be
 CC administered therapeutically, especially by expressing encoding
 CC polynucleotides, e.g. in therapeutic compositions. They can be used to
 CC screen for PRO polypeptide antagonists and agonists useful to identify
 CC drug candidates. They can also be used to produce antibodies, useful to
 CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
 CC therapeutically (e.g. as antagonists or to target and/or deliver
 CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
 CC produce antisense sequences to inhibit polypeptide production. They can
 CC be used to produce probes and primers useful to detect or isolate
 CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
 CC to generate transgenic animals. ABG91355-ABG91363 represent human PRO
 CC amino acid sequences of the invention
 XX SQ Sequence 310 AA;
 Query Match 86.3%; Score 1409; DB 5; Length 310;
 Best Local Similarity 85.8%; Pred. No. 1.1e-104;
 Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MALSRRLRLVRLVRLPHFLLPRGCMIEAVNLKSSNRNPVWHEPESVLSCLITTSQT 60
 DB 1 MALRRPRLRLCARLPDFLLPRGCLIGAVNLKSSNRTPVQEFESVLSCLITTSQT 60
 QY 61 SDPRIEMKKIQDQTTVVYFDNKIQDLAGRTDVGKTSLRIMNVTSDSAIYRCEVVAL 120
 DB 61 SDPRIEMKKIQDQTTVVYFDNKIQDLAGRTDVGKTSLRIMNVTSDSAIYRCEVVAL 120
 QY 121 NDRKEVDEITELIVQKVPVPCRPAAVPGVKATLQCESEGYRPHYSWRNDVPL 180
 DB 121 NDRKEIDBIIVILTVQKVPVPCRPAAVPGVKATLQCESEGYRPHYSWRNDVPL 180
 QY 181 PTDSRANPRFNSFFVNSVETGLVFNVAHKDSDGQYICIASNDAGAACRCEQDMEVYDL 240
 DB 181 PTDSRANPRFNSFFVNSVETGLVFNVAHKDSDGQYICIASNDAGAACRCEQDMEVYDL 240
 QY 241 NIAGIIGGVLLVILAVITWIGICCAVRRCFISKQDGSYKSPGKHGCVNVRTSEEG 300
 DB 241 NIAGIIGGVLLVILAVITWIGICCAVRRCFISKQDGSYKSPGKHGCVNVRTSEEG 300
 QY 301 DFRHKSFSVI 310
 DB 301 DFRHKSFSVI 310

RESULT 15
 ABG84947
 ID ABG84947 standard; protein; 310 AA.
 XX AC ABG84947;
 XX DT 16-MAY-2002 (first entry)
 XX DE Human PRO1868 protein sequence SEQ ID NO:262.
 XX KW Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
 KW vulnervary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX OS Homo sapiens.
 XX PN WO200200690-A2.
 XX PD 03-JAN-2002.

PP 20-JUN-2001; 2001WO-US019692.
XX 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 28-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US005520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX (GETH) GENENTECH INC.
PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI: 2002-090516/12.
DR N-PSDB; ABL88202.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 262; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABL885003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention

XX Sequence 310 AA;

Query Match 86.3%; Score 1409; DB 5; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

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QY 61 SDPRIEWKKIQDQQTYYVFDNKKIQDLAGRTDVFGRKTSLRIRWVTRSDSAIYRCRYVAL 120
DB 61 SDPRIEWKKIQDQQTYYVFDNKKIQDLAGRAIILGKTSLKIRWVTRSDSALYRCRYVAR 120
QY 121 NDRKEVDEITIELIVQVKPVPVCRIPAAVPVCKTATLQCRSEGYPRPHYSWTRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWTRNDVPL 180
QY 181 PTDSRANPRFQNSPHVNSGTGLVFNVAHKDSDGYTCIASNDAGAARCEGQDMEVYDL 240
DB 181 PTDSRANPRFQNSPHVNSGTGLVFNVAHKDSDGYTCIASNDAGAARCEGQDMEVYDL 240
QY 241 NIAGIIGGVLVVLIVLAVITMGICCAVRRGCFISSKODGESYKSPGKHGQVNYIRTSBEG 300
DB 241 NIGGIIGGVLVVLAVLALITLIGICCAVRRGYFINNKODGESYKSPGKHGQVNYIRTSBEG 300
QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310

Search completed: June 15, 2004, 11:03:06
Job time : 52.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:01:19 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYLPHFL.....VNYIRTSEGDPRHKSFPVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
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5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1409	86.3	310	4	US-09-905-125A-423
3	1409	86.3	310	4	US-09-902-775A-423
4	498	30.5	298	4	US-09-152-060-76
5	478	29.3	312	4	US-09-254-465A-9
6	478	29.3	312	4	US-09-907-794A-64
7	478	29.3	312	4	US-09-905-125A-64
8	478	29.3	312	4	US-09-902-775A-64
9	449.5	27.5	300	4	US-09-254-465A-10
10	415	25.4	299	3	US-09-188-930-331
11	415	25.4	299	4	US-09-462-270-2
12	415	25.4	299	4	US-09-254-465A-1
13	415	25.4	299	4	US-09-312-283C-189
14	415	25.4	299	4	US-09-312-283C-331
15	415	25.4	299	4	US-09-907-794A-119
16	415	25.4	299	4	US-09-905-125A-119
17	415	25.4	299	4	US-09-902-775A-119
18	403	24.7	299	3	US-09-188-930-189
19	381.5	23.4	260	4	US-09-254-465A-23
20	381.5	23.4	263	4	US-09-254-465A-25
21	283	17.3	205	4	US-09-462-270-4
22	242.5	14.8	319	1	US-08-597-495B-22
23	242.5	14.8	319	3	US-09-068-051A-22
24	242.5	14.8	319	4	US-09-336-536-67
25	242.5	14.8	319	4	US-09-254-465A-6
26	240.5	14.7	318	3	US-09-068-051A-32
27	236.5	14.5	270	4	US-09-254-465A-24

Sequence 26, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 1, Appl
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Sequence 39, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 39, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 31, Appl
Sequence 16, Appl

28 236.5 14.5 273 4 US-09-254-465A-26
29 197.5 12.1 387 4 US-09-175-928-2
30 173.5 10.6 365 3 US-08-928-383B-2
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32 172.5 10.6 365 3 US-09-272-496-2
33 172.5 10.6 370 4 US-09-336-536-28
34 171.5 10.5 341 4 US-09-336-536-29
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40 167.5 10.3 394 4 US-09-336-536-39
41 166 10.2 1101 3 US-08-986-485-2
42 163 10.0 313 4 US-09-700-397-4
43 163 10.0 344 4 US-09-700-397-3
44 161.5 9.9 246 4 US-09-336-536-31
45 160 9.8 869 1 US-08-374-834-16

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-17
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-133;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
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Db 1 MALSRPPRLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQBFESVELSCIITHSQ 60
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Db 61 SDPRIWKIODEQTTYYVFNKIQGLAGRTDVGKTSLEIMNVTSDSAIYCEVVAR 120
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Db 181 PTDSRANPRFNSSEPHNSSETGLVFTAVHKKDDSGYYCIASNDAGARCEGQMEVYDL 240
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Db 241 NIAGIIGVLVLIWLVITMGICAVRRGCFINNKQDGESYKSPGKHGDNVYIRTSEEG 300
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RESULT 2
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; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Peoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905.125A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 86.3%; Score 1409; DB 4; Length 310;
Best Local Similarity 85.8%; Pred. No. 1.1e-133;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
Qy 1 MALSRRLRLRYALRPHFPFLLLFRGCMIEAVNLKSSNRNPVVFHESVELSCIITHSQ 60
Db 1 MALSRPPRLRLCARLPDPFLLLFRGCLIGAVNLKSSNRTPVQBFESVELSCIITHSQ 60
Qy 61 SDPRIEWKLIODGOTTYYVFNKIQGLAGRTDVGKTSLEIMNVTSDSAIYCEVVAL 120
Db 61 SDPRIWKIODEQTTYYVFNKIQGLAGRTDVGKTSLEIMNVTSDSAIYCEVVAR 120
Qy 121 NDRKEVDITELIVQVKPVPVCRIPAAVPVGKTATLQCOESGYPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVELTVQVKPVPVCRIPAAVPVGKTATLQCOESGYPHYSWYRNDVPL 180


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; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-64

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Query Match          29.3%; Score 478; DB 4; Length 312;
Best Local Similarity 36.3%; Pred. No. 6.9e-40;
Matches 110; Conservative 62; Mismatches 109; Indels 22; Gaps 8;

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QY  116  EVVALNDR-KVDEITIELIVQKVPYTPVCRIAPAAVPVGKATATLQCOSESGYPRPHYSWY 174
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Db  110  EYSAPEQQONLEEDVTLELVAPVPVCEVPSSALSGTVVLELRQDKEGNPAPETWTP 169

QY  175  RNDVPLPTDSRANPRFQNSFHNSTGLTVFNVAHKDSGGYYCTASNDGAARCEGQD 234
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Db  170  KDGIRLENPRLGSQSTNSYTMNTKGTGLQFNTVSKLDGTGSCARNVGVYRCPGKR 229

QY  235  MEVYDLNIAIGGVVLVLVLAVITWGTCCAYRCGP---TSSKQDGESYKSPGHGCV 291
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Db  230  MQVDDLNISSIIIAVVVVALVIVSGLGVCTAQRKGYSKETSFKQKSSSSKATTMSENV 289

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Db  290  QWL 292

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RESULT 7
US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376

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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Faoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
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; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-64

```

Query Match 29.3%; Score 478; DB 4; Length 312;

	Best Local Similarity	36.3%; Pred.	No. 6.9e-40;		
Matches	110; Conservative	62; Mismatches	109; Indels	22; Gaps	8
Qy	3	LRSRLRQLYARLPHFPFLLLFRGCMW----	EAVLNKSSNRNPVH--EPSESVELSCII	55	
Db	1	MARRSRHL-----LLLLLVYLVALGYHKAYGPSAPKDQQVVTAVEYQEAILAC-K	51		
Qy	56	THSQTSDPRIENWKIKDQGTTYTVDFDNKI QGLAGRTDVFGKTSLRINVTSDSAIYRC	115		
Db	52	TPPKTIVSSRLWEKKL-GRSSVFYYQTLQGDFFKNRAEMI-DENIRINKNTRSDAGRKT	109		
Qy	116	EWALNDR-KEVDITIELILVQVKPVPVCRI PAAPVPVGKTATLCQCSESGVRPHYSWY	174		
Db	110	EVSAPESQGNLEBDVTLEVLA VAPSCEVPSSALS GTTVELRCODKEGNAPEYTWF	169		
Qy	175	RNDVPLPTDSRAPRPONSHFVNSETGL VFNAVHKDDSGYYCIASNDAGAACEQD	234		
Db	170	KDGIRLENPRLGSGNSTSYTNMTKTGTLOFTNTVSKLDTCGEYSCEARNSVG YRPCOKR	229		
Qy	235	MEVYDLNLAIIGGVVLVI LVAIVTMGI CCA YRRGC F---ISSRKDCGESYKS PGKH DGV	291		
Db	230	MQVDDLNI SGIIAAVVVVALVISCG LGVCYAQRKGYESKETSFQKSNSSSKATTMSNV	289		
Qy	292	NYI	294		
Db	290	OWL	292		

RESULT 8

US-09-902-775A-64
: Sequence 64. Application US/09902775A

; Patent No. 6686451
 ; Application 05/899027, USA
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary B.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.

RESULT 9

US-09-254-465A-10
: Sequence 10, Application US/09254465A

Patent No. 6410708
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gunder, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.

```

; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; FILE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1 (US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 10
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-254-465A-10

Query Match 27.5%; Score 449.5; DB 4; Length 300;
Best Local Similarity 34.2%; Pred. No. 4.8e-37;
Matches 102; Conservative 64; Mismatches 117; Indels 15; Gaps 7;

QY 20 LLLFRGCMIEAV-----NLKSNRPVHVHFEVSVELSCIITHSQTSDPRIEWKIQDQ 74
DB 11 LFLFPTSMILSVQKGVYTAQSDVQVPEHSIKLTC--TVSGFSSPRVEMKPVQGST 68
QY 75 TTVVYFDNKIQDLAGRTDVFQKTSLRINWVTRSDSAIYRCEVVALNDRKEVDITIELI 134
DB 69 TALVCNSQITAPYADRV--TFSSGTFVSVTROMGEYTC-MVSEGGQNYGEVSIHUT 126
QY 135 VQVFPVPCRIIPAAVPGVKATLQOESGEGYPRPHYSWYRNDVPLPT-DSRANPRFQNS 193
DB 127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDSPPSEYFWFDGIGSLMTADAKKTRAPMS 186
QY 194 SFHVNSETGLVFNVAHKDSDGOYCIASNDAGAA-RCBQDMEVYDLNIAIGGVLVV 252
DB 187 SFTIDPKSGDLIPDPVTAFTDSGSEYTCQAQNGYGTAMRSEAAHMDAVELNVGGIVAALVT 246
QY 253 LVLAVITMGICCAVRRGCFISSKQDGESYKSPGKHGDNVYIRTS-BEGDPRHKSSPVI 310
DB 247 LILLGLLIFGVWFAYSRGIFETIKG-----TAPKKVYISQPSRSEGEFKQTSPLV 300

RESULT 10
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-331

Query Match 25.4%; Score 415; DB 3; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;

QY 18 FFLLLFRGCMIEAVNLKSNRPVHVHFEVSVELSCIITHSQTSDPRIEWKIQDQTTY 77
DB 15 FILAILLCSLALGCVTVHSEPEVRIPENNPVKLSC--AYSGFSSPRVEMKFKDQDITRL 72
QY 78 VYFDNKIQDLAGRTDVFQKTSLRINWVTRSDSAIYRCEVVALNDRKEVDITIELIVQV 137
DB 73 VCYNNKITASYEDRV--TFLPTGITPKSVTRDGTGYTC-MVSEGGNSYGEVKVLIIVL 130
QY 138 KPVTVPVCRIPAAVPGVKATLQOESGEGYPRPHYSWYRNDVPLPTDSRANPRFQNSP 197
DB 131 PPSKPTVNIPSSATIGNRAVLTCSEQDGGSPSEYTFWFGDGIWMPNPKSTRAFNSSYVL 190
QY 198 NSETGLVFNVAHKDSDGOYCIASNDAGAAARCEGQ-DMEVYDLNIAIGGVLVVLI 256
DB 191 NPTTGLVFDPLSASDTGEYSCEARNGYGTPTMTSNVARMVAVRNVGVIAAVALVTILL 250
QY 257 AVITMGICCAVRRGCFISSKQDGESYKSPGKHGDNVYIRTS--BEGDPRHKSSPVI 310
DB 251 GILVFGIWFAYSRGHFDRTKKGTSKK-----VIYQSPSARSEGEFKQTSPLV 299

RESULT 12
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.

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DB 15 FILAILLCSLALGCVTVHSEPEVRIPENNPVKLSC--AYSGFSSPRVEMKFKDQDITRL 72
QY 78 VYFDNKIQDLAGRTDVFQKTSLRINWVTRSDSAIYRCEVVALNDRKEVDITIELIVQV 137
DB 73 VCYNNKITASYEDRV--TFLPTGITPKSVTRDGTGYTC-MVSEGGNSYGEVKVLIIVL 130
QY 138 KPVTVPVCRIPAAVPGVKATLQOESGEGYPRPHYSWYRNDVPLPTDSRANPRFQNSP 197
DB 131 PPSKPTVNIPSSATIGNRAVLTCSEQDGGSPSEYTFWFGDGIWMPNPKSTRAFNSSYVL 190
QY 198 NSETGLVFNVAHKDSDGOYCIASNDAGAAARCEGQ-DMEVYDLNIAIGGVLVVLI 256
DB 191 NPTTGLVFDPLSASDTGEYSCEARNGYGTPTMTSNVARMVAVRNVGVIAAVALVTILL 250
QY 257 AVITMGICCAVRRGCFISSKQDGESYKSPGKHGDNVYIRTS--BEGDPRHKSSPVI 310
DB 251 GILVFGIWFAYSRGHFDRTKKGTSKK-----VIYQSPSARSEGEFKQTSPLV 299

RESULT 11
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human FII Antigen: A Cell Surface
; FILE OF INVENTION: Receptor Involved in Platelet Aggregation
; FILE REFERENCE: GH-70150US
; CURRENT APPLICATION NUMBER: US/09/462,270
; PRIOR FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-2

Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;

QY 18 FFLLLFRGCMIEAVNLKSNRPVHVHFEVSVELSCIITHSQTSDPRIEWKIQDQTTY 77
DB 15 FILAILLCSLALGCVTVHSEPEVRIPENNPVKLSC--AYSGFSSPRVEMKFKDQDITRL 72
QY 78 VYFDNKIQDLAGRTDVFQKTSLRINWVTRSDSAIYRCEVVALNDRKEVDITIELIVQV 137
DB 73 VCYNNKITASYEDRV--TFLPTGITPKSVTRDGTGYTC-MVSEGGNSYGEVKVLIIVL 130
QY 138 KPVTVPVCRIPAAVPGVKATLQOESGEGYPRPHYSWYRNDVPLPTDSRANPRFQNSP 197
DB 131 PPSKPTVNIPSSATIGNRAVLTCSEQDGGSPSEYTFWFGDGIWMPNPKSTRAFNSSYVL 190
QY 198 NSETGLVFNVAHKDSDGOYCIASNDAGAAARCEGQ-DMEVYDLNIAIGGVLVVLI 256
DB 191 NPTTGLVFDPLSASDTGEYSCEARNGYGTPTMTSNVARMVAVRNVGVIAAVALVTILL 250
QY 257 AVITMGICCAVRRGCFISSKQDGESYKSPGKHGDNVYIRTS--BEGDPRHKSSPVI 310
DB 251 GILVFGIWFAYSRGHFDRTKKGTSKK-----VIYQSPSARSEGEFKQTSPLV 299

RESULT 12
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.

```

APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austen L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P1216R1(US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIORITY APPLICATION NUMBER: PCT/US98/24055
PRIORITY FILING DATE: 1998-11-20
PRIORITY APPLICATION NUMBER: US 60/066,364
PRIORITY FILING DATE: 1997-11-21
PRIORITY APPLICATION NUMBER: US 60/078,936
PRIORITY FILING DATE: 1998-03-20
PRIORITY APPLICATION NUMBER: PCT/US98/19437
PRIORITY FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 1
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-1

Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;
Qy 18 PFLLLFGCMIEAVNLKSSNNPVVHFEPSVLSCLIIHSTQSDPRIEMKKIQDQTTY 77
Db 15 FILAILLCSALGVSIVHSSSEPEVRIPENNPKLSC--AYSGFSSPRVEMKPDQDTRL 72
Qy 78 VYFDNKIQDLAGRTDVFCKTSLRIWNVTRSDSAIYRCVVALNDRKVEDEITELIVQV 137
Db 73 VCYNKKITASYEDRV-TFLPTGITFKSVTRDTGYTTC-MVSEEGNSYGEVKVLLIVL 130
Qy 138 KPVTFCVCRIPAAVPVKGKTATLQCSSEGYPRPHYSWYRNDVPLPDTSDRANPRQNSSFHV 197
Db 131 PPSKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTFWKGIVMPTNPKSTRAFSSSYVL 190
Qy 198 NSETGTLVFNHVKDDSGOYCIANDAGAACRCEQ-DMEVVDNLNAGIIGVLLVVL 256
Db 191 NPTTGELVDFPLASDGTGEYSCEARNGYGTPTMSNAVRMEAVERNVGVIAVAVLTLILL 250
Qy 257 AVITWGICCAVRRGCFISSKQDGBSYKSPGKHGDNVYIRTS--REGDFRHKSFVI 310
Db 251 GILVFGIWFAYSRGHFDRTKGTSSKK-----VIYQPSARSSEGEFQTSFLV 299

RESULT 13
US-09-312-283C-189
Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 189
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse

US-09-312-283C-189

Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;
Qy 18 PFLLLFGCMIEAVNLKSSNNPVVHFEPSVLSCLIIHSTQSDPRIEMKKIQDQTTY 77
Db 15 FILAILLCSALGVSIVHSSSEPEVRIPENNPKLSC--AYSGFSSPRVEMKPDQDTRL 72
Qy 78 VYFDNKIQDLAGRTDVFCKTSLRIWNVTRSDSAIYRCVVALNDRKVEDEITELIVQV 137
Db 73 VCYNKKITASYEDRV-TFLPTGITFKSVTRDTGYTTC-MVSEEGNSYGEVKVLLIVL 130
Qy 138 KPVTFCVCRIPAAVPVKGKTATLQCSSEGYPRPHYSWYRNDVPLPDTSDRANPRQNSSFHV 197
Db 131 PPSKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTFWKGIVMPTNPKSTRAFSSSYVL 190
Qy 198 NSETGTLVFNHVKDDSGOYCIANDAGAACRCEQ-DMEVVDNLNAGIIGVLLVVL 256
Db 191 NPTTGELVDFPLASDGTGEYSCEARNGYGTPTMSNAVRMEAVERNVGVIAVAVLTLILL 250
Qy 257 AVITWGICCAVRRGCFISSKQDGBSYKSPGKHGDNVYIRTS--REGDFRHKSFVI 310
Db 251 GILVFGIWFAYSRGHFDRTKGTSSKK-----VIYQPSARSSEGEFQTSFLV 299

RESULT 14

US-09-312-283C-331
Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 331
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-331

Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;
Qy 18 PFLLLFGCMIEAVNLKSSNNPVVHFEPSVLSCLIIHSTQSDPRIEMKKIQDQTTY 77
Db 15 FILAILLCSALGVSIVHSSSEPEVRIPENNPKLSC--AYSGFSSPRVEMKPDQDTRL 72
Qy 78 VYFDNKIQDLAGRTDVFCKTSLRIWNVTRSDSAIYRCVVALNDRKVEDEITELIVQV 137
Db 73 VCYNKKITASYEDRV-TFLPTGITFKSVTRDTGYTTC-MVSEEGNSYGEVKVLLIVL 130
Qy 138 KPVTFCVCRIPAAVPVKGKTATLQCSSEGYPRPHYSWYRNDVPLPDTSDRANPRQNSSFHV 197
Db 131 PPSKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTFWKGIVMPTNPKSTRAFSSSYVL 190
Qy 198 NSETGTLVFNHVKDDSGOYCIANDAGAACRCEQ-DMEVVDNLNAGIIGVLLVVL 256
Db 191 NPTTGELVDFPLASDGTGEYSCEARNGYGTPTMSNAVRMEAVERNVGVIAVAVLTLILL 250
Qy 257 AVITWGICCAVRRGCFISSKQDGBSYKSPGKHGDNVYIRTS--REGDFRHKSFVI 310

Db 251 GILVFGIMFAYSRGHFDRTKGTSSKK-----VIYSQPSARSEGEFKQTSSFLV 299

RESULT 15

US-09-907-794A-119

Sequence 119, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kiljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 119

; LENGTH: 299

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-907-794A-119

Query Match 25.4%; Score 415; DB 4; Length 299;

Best Local Similarity 33.8%; Pred.No.1.4e-33;

Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;

QY 18 FELLALLFRGCMIEAVNLKSSNPNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDQOTTY 77

DB 15 FILAILLCSLALGSVTVHSSEBEVRIPENNPVKLSC--AYSGFSSPRVEMKPDQGDTRL 72

QY 78 VYFDNKIQGDLAGRTDVPKTSRLRIWNVTRSDSAIYRCVAVLNDKREVDRIELIVQV 137

DB 73 VCYNKRITASYEDRV--TFLPTGITFKSVTREDTGTTC-MVSEGGNSYGEVVKLIVLV 130

QY 138 KPTVPVCRIIPAAVPVCKTATLQOESSEGYRPHYSKVRNDVPLPTDSRANPRFQNSSFHV 197

DB 131 PESKPTVNIPSSATIGNRAVLTCSEODGSPFSEYTWKDGIVMPTMPKSTRAFNSSYVL 190

QY 198 NSETGLTVFNVAHKDDSGOYYCIASNDAGAARCEGQ-DMEVYDLNIAIGIIGVVLVILV 256

DB 191 NPTTGLVDFDPLSASDTGEYSCEARNGYGTPTMSNAVRMEAVERNVGVIAAIVLTILL 250

QY 257 AVITMGICCAIYRRCGCPFISSKQDGBSYKSPCKHGDVNYIRTS--EBGDPRHKSSFVI 310

DB 251 GILVFGIMFAYSRGHFDRTKGTSSKK-----VIYSQPSARSEGEFKQTSSFLV 299

Search completed: June 15, 2004, 11:06:31

Job time : 17.5 secs

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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:03:14 ; Search time 39 Seconds
(without alignments)
2239.361 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLVRLPHFL.....VNYRTSSEGRFHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1409	86.3	310	9 US-09-909-320-423	Sequence 423, App
2	1409	86.3	310	9 US-09-909-088B-423	Sequence 423, App
3	1409	86.3	310	9 US-09-905-291A-423	Sequence 423, App
4	1409	86.3	310	9 US-09-902-853-423	Sequence 423, App
5	1409	86.3	310	9 US-09-907-824-423	Sequence 423, App
6	1409	86.3	310	9 US-09-907-841-423	Sequence 423, App
7	1409	86.3	310	10 US-09-904-011-423	Sequence 423, App
8	1409	86.3	310	10 US-09-906-742-423	Sequence 423, App
9	1409	86.3	310	10 US-09-906-838-423	Sequence 423, App
10	1409	86.3	310	10 US-09-907-613-423	Sequence 423, App
11	1409	86.3	310	10 US-09-907-942-423	Sequence 423, App
12	1409	86.3	310	10 US-09-904-859-423	Sequence 423, App
13	1409	86.3	310	10 US-09-909-204-423	Sequence 423, App
14	1409	86.3	310	10 US-09-904-820-423	Sequence 423, App
15	1409	86.3	310	10 US-09-904-786-423	Sequence 423, App

16	1409	86.3	310	10 US-09-906-646-423	Sequence 423, App
17	1409	86.3	310	10 US-09-906-700-423	Sequence 423, App
18	1409	86.3	310	10 US-09-903-786-423	Sequence 423, App
19	1409	86.3	310	10 US-09-902-903-423	Sequence 423, App
20	1409	86.3	310	10 US-09-903-749A-423	Sequence 423, App
21	1409	86.3	310	10 US-09-904-119-423	Sequence 423, App
22	1409	86.3	310	10 US-09-904-956-423	Sequence 423, App
23	1409	86.3	310	10 US-09-902-736-423	Sequence 423, App
24	1409	86.3	310	10 US-09-907-794-423	Sequence 423, App
25	1409	86.3	310	10 US-09-903-943-423	Sequence 423, App
26	1409	86.3	310	10 US-09-904-463-423	Sequence 423, App
27	1409	86.3	310	10 US-09-907-925-423	Sequence 423, App
28	1409	86.3	310	10 US-09-902-692-423	Sequence 423, App
29	1409	86.3	310	10 US-09-903-520-423	Sequence 423, App
30	1409	86.3	310	10 US-09-905-056-423	Sequence 423, App
31	1409	86.3	310	10 US-09-909-064-423	Sequence 423, App
32	1409	86.3	310	10 US-09-904-553-423	Sequence 423, App
33	1409	86.3	310	10 US-09-905-381-423	Sequence 423, App
34	1409	86.3	310	10 US-09-905-088-423	Sequence 423, App
35	1409	86.3	310	10 US-09-907-575-423	Sequence 423, App
36	1409	86.3	310	10 US-09-905-075-423	Sequence 423, App
37	1409	86.3	310	10 US-09-902-759-423	Sequence 423, App
38	1409	86.3	310	10 US-09-902-634-423	Sequence 423, App
39	1409	86.3	310	10 US-09-902-713-423	Sequence 423, App
40	1409	86.3	310	10 US-09-907-979-423	Sequence 423, App
41	1409	86.3	310	10 US-09-902-615-423	Sequence 423, App
42	1409	86.3	310	10 US-09-903-925-423	Sequence 423, App
43	1409	86.3	310	10 US-09-906-760A-423	Sequence 423, App
44	1409	86.3	310	10 US-09-903-823-423	Sequence 423, App
45	1409	86.3	310	10 US-09-907-652-423	Sequence 423, App

ALIGNMENTS

RESULT 1

US-09-909-320-423
; Sequence 423, Application US/09090320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-423

Query Match 86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MALSRRLRLYLARLPHFFLLLRGQWIEAVNLKSNRPVHVHESVLSCLITHSQ 60
Db 1 MALSRRLRLYLARLPHFFLLLRGQWIEAVNLKSNRPVHVHESVLSCLITHSQ 60
Qy 61 SDPRIWKIKQDQTTVYVFDNKKIQDLGRDTPVGRKTSLRIMNVTRSDSAIYRCEYVAL 120
Db 61 SDPRIWKIKQDQTTVYVFDNKKIQDLGRDTPVGRKTSLRIMNVTRSDSAIYRCEYVAL 120
Qy 121 NDRKEVDIEITELIVQKPTVPCRIIPAAVPVGHKTATLQCESGCPYRPHYSWYRNDVPL 180
Db 121 NDRKEVDIEITELIVQKPTVPCRIIPAAVPVGHKTATLQCESGCPYRPHYSWYRNDVPL 180
Qy 181 PTDSRANPRFNSFHVNSSETGLVFNVAHVKDDSGQYVCIASNDAGARCEGDMEVYDL 240
Db 181 PTDSRANPRFNSFHVNSSETGLVFNVAHVKDDSGQYVCIASNDAGARCEGDMEVYDL 240
Qy 241 NIAGIIGGLVAVLVLAVITWIGICAYRRCCTISSKQDGSYKSPGKHGDGVNVRTSEB 300
Db 241 NIAGIIGGLVAVLVLAVITWIGICAYRRCCTISSKQDGSYKSPGKHGDGVNVRTSEB 300
Qy 301 DFRHKSFSVI 310
Db 301 DFRHKSFSVI 310

RESULT 2
US-09-909-088B-423
; Sequence 423, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-088B-423

Query Match 86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRLRLRLYLARLPHFLLFRGCMIEAVNLKSSNRNPVVHBFESVELSCIITHSQT 60
DB 1 MALSRLRLRLCARLPDPFLLFRGLIGAVNLKSSNRTPVQVFPESVELSCIITDSQT 60
QY 61 SDPRIEMKKIQDQTYTVFNDKIQDLAGRTDVGKTSRLTNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIEMKKIQDQTYTVFNDKIQDLAGRAIILGKTSKLTNNVTRSDSAIYRCEVVAR 120
QY 121 NDRKEVDEITIELIVQVKPVPVCRIPAAVPVVKATLQCESEGVPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVELTVQVKPVPVCRIPAAVPVVKATLQCESEGVPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFONSSPHVNSSETGLVFNVAHKKDSQYTCIASNDAGARCEQDMVYDL 240
DB 181 PTDSRANPRFONSSPHVNSSETGLVFNVAHKKDSQYTCIASNDAGARCEQDMVYDL 240
QY 241 NIAGIIGVVLVILVAVITMGIICAYRRCGCFISSQDGSYKSPGKHGCVNIRTSEB 300
DB 241 NIAGIIGVVLVILVAVITMGIICAYRRCGCFISSQDGSYKSPGKHGCVNIRTSEB 300
QY 301 DFRHSSFVI 310
DB 301 DFRHSSFVI 310

RESULT 3
US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-423
Query Match 86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118; Mismatches 26; Indels 0; Gaps 0;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
QY 1 MALSRLRLRLYLARLPHFLLFRGCMIEAVNLKSSNRNPVVHBFESVELSCIITHSQT 60
DB 1 MALSRLRLRLCARLPDPFLLFRGLIGAVNLKSSNRTPVQVFPESVELSCIITDSQT 60
QY 61 SDPRIEMKKIQDQTYTVFNDKIQDLAGRTDVGKTSRLTNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIEMKKIQDQTYTVFNDKIQDLAGRAIILGKTSKLTNNVTRSDSAIYRCEVVAR 120
QY 121 NDRKEVDEITIELIVQVKPVPVCRIPAAVPVVKATLQCESEGVPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVELTVQVKPVPVCRIPAAVPVVKATLQCESEGVPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFONSSPHVNSSETGLVFNVAHKKDSQYTCIASNDAGARCEQDMVYDL 240
DB 181 PTDSRANPRFONSSPHVNSSETGLVFNVAHKKDSQYTCIASNDAGARCEQDMVYDL 240
QY 241 NIAGIIGVVLVILVAVITMGIICAYRRCGCFISSQDGSYKSPGKHGCVNIRTSEB 300
DB 241 NIAGIIGVVLVILVAVITMGIICAYRRCGCFISSQDGSYKSPGKHGCVNIRTSEB 300
QY 301 DFRHSSFVI 310
DB 301 DFRHSSFVI 310
RESULT 4
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-902-853-423

Query Match      86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy      1 MALSRRLRLRYALRPHFLILLFGCMIEAVNLKSSNNRPVWHEFESVLSCLITHSQT 60
Db      1 MALRRPRLRLCARLPDFLLILLFGCLIGAVNLKSSNRPVWQEFESVLSCLITDSQT 60

Qy      61 SDPRIWKKIQDQOTYYVFNKIQGLAGRTDVPKTSLSIWNVTRSDSAIYRCEVVAL 120
Db      61 SDPRIWKKIQDEQTYVFNKIQGLAGRAEILGKTSLSIWNVTRSDSAIYRCEVVAR 120

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-902-853-423

; Sequence 423, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-824-423

Query Match      86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRLRLRLVARLPHFLLLLFRGCMTEAVNLKSNRPVHVHBFESVELSCIITHSQT 60
Db 1 MALRRPRLRLCARLPDFLLLLFRGLICAVNLKSNRTPVQBFESVELSCIITHSQT 60
QY 61 SDPRIEMKKIQDQTTVVYFDNKKIQDLAGRTDVPCKTSLRIWNVTRSDAIVRCVVAL 120
Db 61 SDPRIEMKKIQDQTTVVYFDNKKIQDLAGRTDVPCKTSLRIWNVTRSDAIVRCVVAR 120
QY 121 NDRKEVDEITIELIVQKVPVPCRIAPAAVPVGKTATLQCSSEGYPVPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQKVPVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFNSPHVNSSETGLVFNVAHKDSDGQYCIASNDAGARCEQDMVEYDL 240
Db 181 PTDSRANPRFNSPHVNSSETGLVFNVAHKDSDGQYCIASNDAGARCEQDMVEYDL 240
QY 241 NIAGIIGGVLVNLVLAITWGIICCAVRGCTSSKQDSYKSPCKHGDGVNVRTSEEG 300
Db 241 NIAGIIGGVLVNLVLAITWGIICCAVRGCTSSKQDSYKSPCKHGDGVNVRTDEEG 300
QY 301 DFRHKSSFVI 310
Db 301 DFRHKSSFVI 310

RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
```

```
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-841-423

Query Match      86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRLRLRLVARLPHFLLLLFRGCMTEAVNLKSNRPVHVHBFESVELSCIITHSQT 60
Db 1 MALRRPRLRLCARLPDFLLLLFRGLICAVNLKSNRTPVQBFESVELSCIITHSQT 60
QY 61 SDPRIEMKKIQDQTTVVYFDNKKIQDLAGRTDVPCKTSLRIWNVTRSDAIVRCVVAL 120
Db 61 SDPRIEMKKIQDQTTVVYFDNKKIQDLAGRTDVPCKTSLRIWNVTRSDAIVRCVVAR 120
QY 121 NDRKEVDEITIELIVQKVPVPCRIAPAAVPVGKTATLQCSSEGYPVPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQKVPVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFNSPHVNSSETGLVFNVAHKDSDGQYCIASNDAGARCEQDMVEYDL 240
Db 181 PTDSRANPRFNSPHVNSSETGLVFNVAHKDSDGQYCIASNDAGARCEQDMVEYDL 240
QY 241 NIAGIIGGVLVNLVLAITWGIICCAVRGCTSSKQDSYKSPCKHGDGVNVRTSEEG 300
Db 241 NIAGIIGGVLVNLVLAITWGIICCAVRGCTSSKQDSYKSPCKHGDGVNVRTDEEG 300
QY 301 DFRHKSSFVI 310
Db 301 DFRHKSSFVI 310

RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011
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Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien

US-09-904-011-423
Query Match 86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRRLRLRLYLARLPEPFLILLPRGOMIRAVNLKSSNRNPVVHVFESVLSCLITHSQT 60
DB 1 MALRRPPLRLRLCARLPDFFULLFRGCLIGAVNLKSSNRTPVVQVFESVLSCLITDSQT 60
QY 61 SDPRIEMKKIQDQQTYYVFDNKKIQGLAGRTDVFGKTSLEIMNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIEMKKIQDQQTYYVFDNKKIQGLAGRTDVFGKTSLEIMNVTRSDSAIYRCEVVAL 120
QY 121 NDRKVDREITIELIVQVKPTVPVCRIPAAVPVGTATLOQESSEGYRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPVCRIPAAVPVGTATLOQESSEGYRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFNGSFHVNSETGLVFNVAHKDQGYVCIAASNDAGAACRCEQDMEVYDL 240
DB 181 PTDSRANPRFNGSFHVNSETGLVFNVAHKDQGYVCIAASNDAGAACRCEQDMEVYDL 240
QY 241 NIAGIIGGVLVVLVLAVITMGICCAVRRGCFISSKODGESYKSPGKHGDNVYIRTSBEG 300
DB 241 NIAGIIGGVLVVLVLAVITMGICCAVRRGCFISSKODGESYKSPGKHGDNVYIRTSBEG 300
QY 301 DFRHKSSEFVI 310
DB 301 DFRHKSSEFVI 310

RESULT 8
US-09-906-742-423
Sequence 423, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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Qy	1	MALSRRLRLRYARLPHFLILLFRGCMIEAVNLKSSNNRPVPHFPESVELSCIITHSQT	60
Db			
Db	1	MALRRPPLRLCARLPDPFLILLFRGLIGAVNLKSSNRPVQBPESVELSCIITDSQT	60
Qy	61	SDPRIENKKIODGQTTVVYFONKIOGDLAGRDTVFGKTSLRINWTRSDAISYRCFVVAL	120
Db			
Db	61	SDPRIENKKIQDEQTTVYFFONKIOGDLAGRABIIIGKTSKLTINWTRDSALYRCFVWAR	120
Qy	121	NDRKEVDIBITIELIVQVRPVPVCRIPAAVPVGKTAITLQCSSEGYRPHYSYWRNDVPL	180
Db			
Db	121	NDRKEIDBIVIELTVQVRPVPVCRVPRKAVPVGMATLHCQSSSEGHPRPHYSYWRNDVPL	180
Qy	181	PTDSRANRPNRPNSSPHVNSGTGLVPNAVHKDDSGYYCIASNDAGAACRCEQDMVEYDL	240
Db			
Db	181	PTDSRANRPNRPNSSPHLNSGTGLVFTAVHKDDSGYYCIASNDAGSARCEQEVEYDL	240
Qy	241	NIAGIIGGLVVLVILAVITMGICCAAYRRCGCFISSKQDGESYKSPGKHDPGVNVRTSEB	300
Db			
Db	241	NIGGIIGGLVVLVAVLALITGICCAAYRGRYFINNKQDGESYKNPGKPGGVNVRTDEB	300
Qy	301	DFRHKSSPVI	310
Db			
Db	301	DFRHKSSPVI	310

RESULT 10

US-09-907-613-423
Sequence 423, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13

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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-423

Query Match      86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy      1  MALSRRLRLRYARLPHPFLLLLPRGCMIRAVNLKSNRNPPVHPEFESVLSCLIIHQSQT 60
Db      1  MALRRPRLRLCARLPDPFLLLLPRGLICAVNLKSNRTPVQEFESVLSCLIIHQSQT 60

Qy      61  SDPRIEMKKIQDQGTYYVYFNDKIQDGLAGRTDVPFGKTSLSLRINNVTRSDSAIYRCFVVAL 120
Db      61  SDPRIEMKKIQDQGTYYVYFNDKIQDGLAGRAEILGKTSLSLRINNVTRSDSAIYRCFVVAR 120

Qy      121  NDRKEVDSEIYELIVQVKPTVPVCRPAAPVPGKATATLCOESEGYPHPHYSWRNDVPL 180
Db      121  NDRKEIDSEIYELIVQVKPTVPVCRVPAVPVGKMATLHCQSEGHPRPHYSWRNDVPL 180

Qy      181  PTDSRANPRFONSFFHNSETGLVFNAVHKDDSGQVYCIASNDAGAARCEGQDMEVYDL 240
Db      181  PTDSRANPRFNSFFHNSGTGLVFTAVHKDDSGQYVYCIASNDAGSARCEEQEMEYVDL 240

Qy      241  NIAGIIGGVLVVLIVLAVITMGICCAAYRCGPISSKQDGESYKSPGKHGQVNYIRTSBBG 300
Db      241  NIGGIIGGVLVVLAVLALITGLICCAAYRCGYPINNKGQDGSYKNPGKPGDGVNIRTDDEG 300

Qy      301  DFRHKSFSVI 310
Db      301  DFRHKSFSVI 310

RESULT 11
US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US200300271146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

```

```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-423

Query Match      86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRRLRLRLYLPHFLLLLPRGCMIEAVNLKSNRPVYHFESEVLSCLIIHDSQT 60
DB 1 MALRRPRLRLCARLDFLLFRGLGAVNLKSNRPVYHFESEVLSCLIIHDSQT 60
QY 61 SDPRIEMKKIQDQQTYYVFDNKKIQDLAGRTDVGKTSRLRIWNVTRSDSAIYRCEVVAL 120
DB 61 SDPRIEMKKIQDQQTYYVFDNKKIQDLAGRAELGKTSRLRIWNVTRSDSAIYRCEVVAR 120

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; Sequence 423, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Pong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
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; PRIOR FILING DATE: 1999-07-07
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; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-904-859-423

Query Match      86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLPHFFLLFRGCMIEAVNLKSSNRNPVHFEFVELSCLIIHST 60
Db 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCLII 60

Qy 61 SDPRIEWKKIQDQTTTYPVFNKIQDLAGRTDVGKTSRLRWVTRSDSALYRCE 120
Db 61 SDPRIEWKKIQDQTTTYPVFNKIQDLAGRTDVGKTSRLRWVTRSDSALYRCE 120

Qy 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180
Db 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180

Qy 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180
Db 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180

Qy 181 PTDSRANPRFNSSPHVNSGTGLVFNVAHKDDSGQYYCIAASNDAGAACRCEQDME 240
Db 181 PTDSRANPRFNSSPHVNSGTGLVFNVAHKDDSGQYYCIAASNDAGAACRCEQDME 240

Qy 241 NIAGIGGVLVAVLAVITWGIICAVRGCFFISSKQDGRSKPGKHGDNVYIRTDE 300
Db 241 NIAGIGGVLVAVLAVITWGIICAVRGCFFISSKQDGRSKPGKHGDNVYIRTDE 300

Qy 301 DFRHKSSPVI 310
Db 301 DFRHKSSPVI 310
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RESULT 13
US-09-909-204-423
; Sequence 423, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
```

```
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCES: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
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; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-204-423

Query Match      86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLPHFFLLFRGCMIEAVNLKSSNRNPVHFEFVELSCLIIHST 60
Db 1 MALRRPRLRLCARLPDFLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCLII 60

Qy 61 SDPRIEWKKIQDQTTTYPVFNKIQDLAGRTDVGKTSRLRWVTRSDSALYRCE 120
Db 61 SDPRIEWKKIQDQTTTYPVFNKIQDLAGRTDVGKTSRLRWVTRSDSALYRCE 120

Qy 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180
Db 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180

Qy 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180
Db 121 NDRKEVDITIELIVQVKPVPVCKRIPAAVPGVKATLQCESEGYPRPHYSWYRND 180

Qy 181 PTDSRANPRFNSSPHVNSGTGLVFNVAHKDDSGQYYCIAASNDAGAACRCEQDME 240
Db 181 PTDSRANPRFNSSPHVNSGTGLVFNVAHKDDSGQYYCIAASNDAGAACRCEQDME 240
```


Tue Jun 15 14:20:05 2004

```
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-786-423

Query Match      86.3%; Score 1409; DB 10; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLPHFFLLLLFRGCMIEAVNLKSNRNPNVHEFESVELSCIITHSQT 60
Db 1 MALRRPPRLRLCARLPDFLLFRGCLLGAVNLKSNRTPVQEFESVELSCIITDSQT 60

Qy 61 SDPRIWKKIQQGQTYVYFDNKIQGDLACRTDVPKTSLEIWNVTRSDSAIYCEVVAL 120
Db 61 SDPRIWKKIQQGQTYVYFDNKIQGDLACRTDVPKTSLEIWNVTRSDSAIYCEVVAL 120

Qy 121 NDRKEVDSEITELIVQKPTPVCRIPAAVPVGTATLQCOESGYPHPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQVAPVTPVCRVPAVPVGTATLQCOESGHPHPHYSWYRNDVPL 180

Qy 181 PTDSRANPRFNSSPHNSSETGTLVFNVAHVHSDGQYYCIASNDAGARCEQDMEVYDL 240
Db 181 PTDSRANPRFNSSPHLNSSETGTLVFTAVHVDSDGQYYCIASNDAGSARCEQEMEVYDL 240

Qy 241 NIAGIIGGLVVLIVLAVITMGICCAVRGCFISSKQDGSYKSPGKHGYNVYRTSEEG 300
Db 241 NIGGIIGGLVVLAVLALITLIGCCAYRRGYFINNKQDGSYKKNPKGPDGVNYIRTDDEG 300

Qy 301 DFRHKSFPVI 310
Db 301 DFRHKSFPVI 310
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Search completed: June 15, 2004, 11:08:01
Job time : 39 secs

Db 251 GILVGIWFPAYSGHFDRTKGTSSKK-----VIYQPSARSGEGBFKQTSFLV 299

RESULT 2

JB0099

neural cell adhesion molecule 1 - African clawed frog

N;Alternate names: NCAM 1

C;Species: Xenopus laevis (African clawed frog)

C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: JB0099

R;Kudo, M.; Takayama, E.; Tadokuma, T.; Shiohawa, K.

Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the major cell-cell adhesion molecules in the brain

A;Reference number: JB0099; MUID:98204770; PMID:9535795

A;Accession: JB0099

A;Molecule type: mRNA

A;Residues: 1-725 <KUD>

A;Cross-references: DDBJ;AB008162; NID:g3116226; PIDN:BA25931.1; PID:g3116227

A;Experimental source: heart

C;Comment: This protein mediates and regulates various cell-cell interactions through both cell-cell and cell-matrix adhesion

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin domain

F;413-475/Domain: immunoglobulin homology <IMM>

F;512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 11.18; Score 181; DB 2; Length 725;

Best Local Similarity 28.81; Pred. No. 7.8e-07;

Matches 60; Conservative 33; Mismatches 81; Indels 34; Gaps 11;

Qy 32 VNLK-----SSNRNPVHVFESVELSCIITHSOTSDPR-IEWK-KIDGGQTTVVYFONKI 84

Db 107 VNLKIYQKLTFFKNAPTQEFEGEDAVIICDVSSIFSIITWRHKGKD-----VIFKQDV 161

Qy 85 QGDLAGRTDVFGRKSLRIMVTRSDSAIYRC--VVALNDRKEVDEITIELIVQKVPVTP 142

Db 162 -----RPVLLANNYLQIRGIKKTDECTYRCGRILA---RGEINYKDIQIVNVNPTIQ 212

Qy 143 V-CRIPAAVPVGTATLQOESGYPHYSWTRNDVPLETDSRANPRFQNSFHVNSE 200

Db 213 ARQLRVNATMAEVSVLSC-DADGFPDPBISLWKGPEIDEGR-----EKISF--NED 263

Qy 201 TGTLVFNAVHKDSDGQYVCIASNDAGAA 228

Db 264 QSEMTIHHVEKDDAEYSCIANNQAGEA 291

RESULT 3

IJXLNL

neural cell adhesion molecule long domain form precursor - African clawed frog

N;Alternate names: NCAM-180

N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C;Accession: S09600

R;Krieg, P.A.; Sakauchi, D.S.; Kintner, C.R.

Nucleic Acids Res. 17, 10321-10335, 1989

A;Title: Primary structure and developmental expression of a large cytoplasmic domain form of NCAM

A;Reference number: S09600; MUID:90098871; PMID:2481269

A;Accession: S09600

A;Molecule type: mRNA

A;Residues: 1-1088 <KRI>

A;Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610

A;Note: The authors translated the codon AAA for residue 970 as Leu

C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM molecule

C;Comment: Several forms of NCAM are produced by alternative splicing.

C;Genetics:

A;Gene: NCAM

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin domain

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <L>

F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status predicted <S>

F;20-705/Domain: extracellular #status predicted <EXT>

F;34-95/Domain: immunoglobulin homology <IMM1>

F;129-188/Domain: immunoglobulin homology <IMM2>

F;149-153/Region: heparin binding #status predicted

F;158-162/Region: heparin binding #status predicted

F;225-284/Domain: immunoglobulin homology <IMM3>

F;317-381/Domain: immunoglobulin homology <IMM4>

F;413-475/Domain: immunoglobulin homology <IMM5>

F;512-589/Domain: fibronectin type III repeat homology <FN3A>

F;618-679/Domain: fibronectin type III repeat homology <FN3B>

F;706-723/Domain: transmembrane #status predicted <TM>

F;724-1088/Domain: intracellular #status predicted <INT>

F;41-93,136-186,232-282,379,420-473/Diulfide bonds: #status predicted

F;219,310,341,417,443,472/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 11.08; Score 180; DB 1; Length 1088;

Best Local Similarity 28.81; Pred. No. 1.5e-06;

Matches 60; Conservative 33; Mismatches 81; Indels 34; Gaps 11;

Qy 32 VNLK-----SSNRNPVHVFESVELSCIITHSOTSDPR-IEWK-KIDGGQTTVVYFONKI 84

Db 107 VNLKIYQKLTFFKNAPTQEFEGEDAVIICDVSSIFSIITWRHKGKD-----VIFKQDV 161

Qy 85 QGDLAGRTDVFGRKSLRIMVTRSDSAIYRC--VVALNDRKEVDEITIELIVQKVPVTP 142

Db 162 -----RPVLLANNYLQIRGIKKTDECTYRCGRILA---RGEINYKDIQIVNVNPTIQ 212

Qy 143 V-CRIPAAVPVGTATLQOESGYPHYSWTRNDVPLETDSRANPRFQNSFHVNSE 200

Db 213 ARQLRVNATMAEVSVLSC-DADGFPDPBISLWKGPEIDEGR-----EKISF--NED 263

Qy 201 TGTLVFNAVHKDSDGQYVCIASNDAGAA 228

Db 264 QSEMTIHHVEKDDAEYSCIANNQAGEA 291

RESULT 4

A39712

kinase-like protein klg precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999

C;Accession: A39712

R;Chou, Y.H.; Hayman, M.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991

A;Title: Characterization of a member of the immunoglobulin gene superfamily that possi

A;Reference number: A39712; MUID:91271300; PMID:1711213

A;Accession: A39712

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1051 <CHO>

A;Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

C;Keywords: ATP

F;775-1046/Domain: protein kinase homology <KIN>

F;783-791/Region: protein kinase ATP-binding motif

Query Match 10.98; Score 178; DB 2; Length 1051;

Best Local Similarity 28.38; Pred. No. 2.1e-06;

Matches 72; Conservative 29; Mismatches 109; Indels 44; Gaps 12;

Qy 45 EP-ESVELSCIITHSOTSDPRIEWKKIQDGGTYYVFDNKKIOGDLAGRTDVFGRKSLRIM 103

Db 496 EFNKEVTVSCATGRE--KPTIQWK-TDG-----SSLPSHVSHRAGI-----LSFH 539

Qy 104 NVTRSDSAIYRCVVALNDRKEVDEITIELIVQKVPVTCRIPAAVPVGTATLQOES 163

Db 540 KVSRSDSNGYTC--IASNSPQGEIRATVQLVAVVYVTFKLEPEPTTVYQGHATMPQCC-A 596

Qy 164 EGYPRPHYSWTRNDVPLETDSRANPRFQNSFHVNSEGTGLVFNAVHKDSDGQYVCIASN 223

Db 597 EGDVPHIQWKGDKIL-DFSKLLPRIQ-----IMPNGSLVIYDVTTEDSGKTCIAGN 649

Qy 224 DA-----GAARCEGQDMEV-YD-LNIAGIIGGVLLVLLVAVITWGICCA 266

Db 650 SCNIKREAFLYVVDKPAASEDEGSSHTPYKMTQITGLSVGAAVAVIIVLGLMFYCKK 709

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 355-364 <RES>

A;Cross-references: GB:M32611; NID:G205643; PIDN:AAA41679.1; PID:G205644

C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM molecule.

C;Comment: Various forms of NCAM are produced by alternative splicing.

C;Genetics:

A;Gene: NCAM

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin superfamily

C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; sIg

P;1-19/Domain: signal sequence #status predicted <SIG>

P;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <EXT>

P;20-721/Domain: extracellular #status predicted <EXT>

P;34-98/Domain: immunoglobulin homology <IMM1>

P;132-191/Domain: immunoglobulin homology <IMM2>

P;152-166/Region: heparin binding #status predicted

P;161-165/Region: heparin binding #status predicted

P;228-290/Domain: immunoglobulin homology <IMM3>

P;263-272/Region: NCAM binding #status predicted

P;323-398/Domain: immunoglobulin homology <IMM4>

P;430-492/Domain: immunoglobulin homology <IMM5>

P;529-606/Domain: fibronectin type III repeat homology <FN3A>

P;635-695/Domain: fibronectin type III repeat homology <FN3B>

P;722-739/Domain: transmembrane #status predicted <TM>

P;740-858/Domain: intracellular #status predicted <INT>

P;41-96,139-189,235-288,330-396,437-490/Diulfide bonds: #status predicted

P;222,316,348,434,460,489/Binding site: carbohydrate (Asn) #status predicted

Query Match 10.6%; Score 172.5; DB 1; Length 858;

Best Local Similarity 27.1%; Pred. No. 4.7e-06;

Matches 61; Conservative 43; Mismatches 84; Indels 37; Gaps 13;

Qy 26 GCMTEA-VNLKSSNR-----NPVVFESVELSCIIITHSQTS-DPRIEWKKIQDQTTVV 78

Db 103 GTQSEATVNVKIFQKLMPKNAPTPQSEKGEDAVICDVVSSLPTTIWK--HKGR--- 156

Qy 79 YFDNKIQGLAGRTDVFQKTSRLNVTNRSDSAIYRC--VVALNDREVDIETILIVQ 136

Db 157 --DVLTKDGV--RPTVLSNNYLQIRKIQDTEGTYCEGRILA---RGEINPKDQIVYN 209

Qy 137 VKPVTVPVCR--IPAAVPVGGKATLCOESGYPHYSWYRNDVPLPLTDSRANPRFQSS 194

Db 210 VPPTVQARQSVNATNLQGSVTLVC-DADGPFPTNSWTKDGEPIENE-----EDDE 262

Qy 195 PHV-NSETGLTVFNAVHKDDSGQYTCIASNDAGAARCEGQDMEVY 238

Db 263 KHIFSDSSSELTIRNVNDKNDEAYVCIENKAGE-----QDASIH 302

RESULT 7

IJMSGNG

neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse

N;Alternate names: NCAM-120

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 31-Dec-2000

C;Accession: A29673; S00382; A44290

R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontana, J. 6, 907-914, 1987

EMBO J. 6, 907-914, 1987

A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000

A;Reference number: A29673; MUID:87246524; PMID:3595563

A;Accession: A29673

A;Molecule type: mRNA

A;Residues: 1-725 <BAR>

A;Cross-references: EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343

P;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.

EMBO J. 7, 625-632, 1988

A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM

A;Reference number: S00382; MUID:88283628; PMID:3396534

A;Accession: S00382

A;Molecule type: DNA

A;Residues: 642-656, 'D', 658-725 <BA2>

A;Cross-references: EMBL:X07195

P;Rougon, G.; Marshak, D.R.

J. Biol. Chem. 261, 3396-3401, 1986
 A;Title: Structural and immunological characterization of the amino-terminal domain of m
 A;Reference number: A44290; MUID:86140120; PMID:3512556
 A;Accession: A44290
 A;Molecule type: protein
 A;Residues: 20-36 <ROU>
 C;Comment: NCM mediates cell-cell adhesion via homophilic binding with another NCM mol
 C;Genetics:
 A;Gene: NCM
 A;Map position: 9
 A;Introns: 701/1
 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;34-98/Domain: immunoglobulin homology <IMM1>
 F;132-191/Domain: immunoglobulin homology <IMM2>
 F;152-156/Region: heparin binding #status predicted
 F;161-165/Region: heparin binding #status predicted
 F;228-290/Domain: immunoglobulin homology <IMM3>
 F;323-388/Domain: NCM binding #status predicted
 F;420-482/Domain: immunoglobulin homology <IMM4>
 F;519-596/Domain: fibronectin type III repeat homology <IMM5>
 F;625-685/Domain: fibronectin type III repeat homology <IMM6>
 F;41-96, 139-189, 235-288, 330-386, 427-480/Diulfide bonds: #status predicted
 F;222, 316, 348, 424, 450, 479/Binding site: carbohydrate (Asn) #status predicted

Query Match 10.4%; Score 169.5; DB 1; Length 725;
 Best Local Similarity 27.7%; Pred. No. 6.8e-06;
 Matches 62; Conservative 43; Mismatches 84; Indels 35; Gaps 13;

Qy 26 GCMIEA-VNLKSSNR-----NPVVHPEFESVELSCIIITHSOTS-DPRIEWKKIQDQTTVV 78
 Db 103 GTQSEATVNVKIFQKLFKNAFTPOEPKGBDAVIVCDVSSLPPTIWK--HKGR--- 156

Qy 79 YFONKIQDGLAGRTDVGKTSRLRWVTRSDSALYRCE--VVALNDRKEVDITIELIVQ 136
 Db 157 --DVILKKDV--RPVLSNNYLQIRGKTKDEGYRCEGRILA---RGEINFKDIQIVVN 209

Qy 137 VKPVTFCR--IPAAVPGVKATATQCESBGYPHYSWTRNDVPLPTDSRANFRQSS 194
 Db 210 VPPTVQARQSIVNATNLQGSVTLVC-DADGFPPTMSWTKDGFPIENEEB-DESRSSV 267

Qy 195 FHVNSGTGLVFNVAHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
 Db 268 ----SDSSEVTIRNVKNDREAYVCIAENKAGE-----QDASIH 302

RESULT 8
 IJMSNL
 neural cell adhesion molecule 1 precursor, long domain splice form - mouse
 N;Alternate names: NCM-180
 N;Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
 C;Accession: A29673; S00844; A28281; A44290; S00383
 R;Barthele, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Pontec
 EMBO J. 6, 907-914, 1987
 A;Title: Isolation and nucleotide sequence of mouse NCM cDNA that codes for a Mr 79,000
 A;Reference number: A29673; MUID:87246524; PMID:3595563
 A;Accession: A29673
 A;Molecule type: mRNA
 A;Residues: 1-548; 'T', 550-571, 'T', 573-574, 'D', 576-588, 'MOPS', 593, 'S', 595-599, 'P', 601, 'L',
 A;Cross-references: EMBL:Y00051; NID:953342; PIDN:CAAG8263.1; PID:953343
 R;Santoni, M.J.; Barthele, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W
 Nucleic Acids Res. 15, 8621-8641, 1987
 A;Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur
 A;Reference number: S00844; MUID:88067687; PMID:3694567
 A;Accession: S00844
 A;Molecule type: mRNA
 A;Residues: 529-809, 1077-1115 <SAN>
 A;Cross-references: EMBL:X06328; NID:953322; PIDN:CAA29641.1; PID:9817984

R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
 EMBO J. 7, 625-632, 1988
 A;Title: Differential splicing and alternative polyadenylation generates distinct NCM
 A;Reference number: S00382; MUID:88283628; PMID:3396534
 A;Accession: S00384
 A;Molecule type: DNA
 A;Residues: 642-1115 <BAR>
 A;Cross-references: EMBL:X07195
 R;Barthele, D.; Vopper, G.; Wille, W.
 Nucleic Acids Res. 16, 4217-4225, 1988
 A;Title: NCM-180, the large isoform of the neural cell adhesion molecule of the mouse,
 A;Reference number: A28281; MUID:88247737; PMID:2454455
 A;Accession: A28281
 A;Molecule type: mRNA
 A;Residues: 804-1081 <BA3>
 A;Cross-references: EMBL:X07244; NID:953321; PIDN:CAA30230.1; PID:9929720
 R;Rougou, G.; Marshak, D.R.
 J. Biol. Chem. 261, 3396-3401, 1986
 A;Title: Structural and immunological characterization of the amino-terminal domain of
 A;Reference number: A44290; MUID:86140120; PMID:3512556
 A;Accession: A44290
 A;Molecule type: protein
 A;Residues: 20-36 <ROU>
 C;Comment: NCM mediates cell-cell adhesion via homophilic binding with another NCM mo
 C;Genetics:
 A;Gene: NCM
 A;Map position: 9
 A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
 C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status exper
 F;20-711/Domain: extracellular #status predicted <EXT>
 F;34-98/Domain: immunoglobulin homology <IMM1>
 F;132-191/Domain: immunoglobulin homology <IMM2>
 F;152-156/Region: heparin binding #status predicted
 F;161-165/Region: heparin binding #status predicted
 F;228-290/Domain: immunoglobulin homology <IMM3>
 F;262-272/Region: NCM binding #status predicted
 F;323-388/Domain: immunoglobulin homology <IMM4>
 F;420-482/Domain: immunoglobulin homology <IMM5>
 F;519-596/Domain: fibronectin type III repeat homology <IMM6>
 F;625-685/Domain: fibronectin type III repeat homology <IMM7>
 F;712-729/Domain: transmembrane #status predicted <TM>
 F;730-1115/Domain: intracellular #status predicted <INT>
 F;41-96, 139-189, 235-288, 330-386, 427-480/Diulfide bonds: #status predicted
 F;222, 316, 348, 424, 450, 479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 169.5; DB 1; Length 1115;
 Best Local Similarity 27.7%; Pred. No. 1.1e-05;
 Matches 62; Conservative 43; Mismatches 84; Indels 35; Gaps 13;

Qy 26 GCMIEA-VNLKSSNR-----NPVVHPEFESVELSCIIITHSOTS-DPRIEWKKIQDQTTVV 78
 Db 103 GTQSEATVNVKIFQKLFKNAFTPOEPKGBDAVIVCDVSSLPPTIWK--HKGR--- 156

Qy 79 YFONKIQDGLAGRTDVGKTSRLRWVTRSDSALYRCE--VVALNDRKEVDITIELIVQ 136
 Db 157 --DVILKKDV--RPVLSNNYLQIRGKTKDEGYRCEGRILA---RGEINFKDIQIVVN 209

Qy 137 VKPVTFCR--IPAAVPGVKATATQCESBGYPHYSWTRNDVPLPTDSRANFRQSS 194
 Db 210 VPPTVQARQSIVNATNLQGSVTLVC-DADGFPPTMSWTKDGFPIENEEB-DESRSSV 267

Qy 195 FHVNSGTGLVFNVAHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
 Db 268 ----SDSSEVTIRNVKNDREAYVCIAENKAGE-----QDASIH 302

RESULT 9
 JE0100

neural cell adhesion molecule 2 - African clawed frog
N:Alternate names: N-CAM 2
C:Species: Xenopus laevis (African clawed frog)
C>Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: J00100
R:Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A:Title: Molecular cloning of ssd-form neural cell
A:Reference number: JE0099; MUID:98204770; PMID:9535795
A:Accession: JE0100
A:Molecule type: mRNA
A:Residues: 1-725 <KUD>
A:Cross-references: DDBJ:AB008163; NID:g3116228; PIDN:BAA25932.1; PID:g3116229
A:Experimental source: heart
C:Comment: This protein mediates and regulates various cell-cell interactions through bo
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
P:413-475/Domain: immunoglobulin homology <IMM>
P:512-589/Domain: fibronectin type III repeat homology <3PR>

Query Match 10.3%; Score 169; DB 2; Length 725;
Best Local Similarity 28.4%; Pred. No. 7.4e-06;
Matches 59; Conservative 33; Mismatches 82; Indels 34; Gaps 11;

QY 32 VNLKSNR-----NPVVHFESEVELSCIITHSOTSDPR-IEWK-KIQDQTTYYVFNKI 84
DB 107 VNLKIYQKLTFTKYAPTPOBFTGEDAVIICDVSSSIPSIITWRHKGK-----VIFPKD 161
QY 85 QGDLAGRTDVGKTSIRIWNVTRSDSAIYRCB--VVALNDRKRVDSITIELIIVOVKPVTP 142
DB 162 -----RFVLANNYLQIRIGIKTKDGNTRCEGRILA---RGKINYKDIQIVNVVPLIQ 212
QY 143 V--CRIPAAVPVGKATLQCOSEGEYPRPHYSYRNDVPLPTDSRANPRFQNSSPHVNSE 200
DB 213 ARQIRVNATNANMDESIVLSC-DADGFPDPEISWLKKGEPEDG-----EKISP--NED 263
QY 201 TGTLVFNVAHKDDSGQYYCIASNDAGAA 228
DB 264 KSEMTIYRVEKDEAEYSCIANNQAGEA 291

RESULT 10
JN0635
neural cell adhesion molecule 2 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C:Accession: JN0635
R:Toniessen, K.F.; Krieg, P.A.
Gene 127, 243-247, 1991
A:Title: Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are ex
A:Reference number: JN0635; MUID:93273239; PMID:7684721
A:Accession: JN0635
A:Molecule type: mRNA
A:Residues: 1-1092 <TON>
A:Cross-references: GB:M76710; NID:g214611; PIDN:AAA49910.1; PID:g214612
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C:Genetics:
A:Gene: NCAM2
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialoglyc
P:1-19/Domain: signal sequence #status predicted <SIG>
P:20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
P:20-705/Domain: extracellular #status predicted <EXT>
P:34-95/Domain: immunoglobulin homology <IMM1>
P:129-188/Domain: immunoglobulin homology <IMM2>
P:149-153/Region: heparin binding #status predicted
P:158-162/Region: heparin binding #status predicted
P:317-381/Domain: immunoglobulin homology <IMM3>
P:413-475/Domain: immunoglobulin homology <IMM4>
P:512-589/Domain: fibronectin type III repeat homology <FN3A>
P:619-680/Domain: fibronectin type III repeat homology <FN3B>
P:706-723/Domain: transmembrane #status predicted <TM>
P:724-1092/Domain: intracellular #status predicted <INT>
P:41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted

P:219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.3%; Score 169; DB 1; Length 1092;
Best Local Similarity 28.4%; Pred. No. 1.2e-05;
Matches 59; Conservative 33; Mismatches 82; Indels 34; Gaps 11;

QY 32 VNLKSNR-----NPVVHFESEVELSCIITHSOTSDPR-IEWK-KIQDQTTYYVFNKI 84
DB 107 VNLKIYQKLTFTKYAPTPOBFTGEDAVIICDVSSSIPSIITWRHKGK-----VIFPKD 161
QY 85 QGDLAGRTDVGKTSIRIWNVTRSDSAIYRCB--VVALNDRKRVDSITIELIIVOVKPVTP 142
DB 162 -----RFVLANNYLQIRIGIKTKDGNTRCEGRILA---RGKINYKDIQIVNVVPLIQ 212
QY 143 V--CRIPAAVPVGKATLQCOSEGEYPRPHYSYRNDVPLPTDSRANPRFQNSSPHVNSE 200
DB 213 ARQIRVNATNANMDESIVLSC-DADGFPDPEISWLKKGEPEDG-----EKISP--NED 263
QY 201 TGTLVFNVAHKDDSGQYYCIASNDAGAA 228
DB 264 KSEMTIYRVEKDEAEYSCIANNQAGEA 291

RESULT 11
S18252
heparan sulfate proteoglycan - mouse
N:Alternate names: perlecan
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S18252; A31917; B31917; S66460
R:Noonan, D.M.; Pullie, A.; Valente, P.; Cal, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Hori
J. Biol. Chem. 266, 22939-22947, 1991
A:Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
adhesion molecule.
A:Reference number: S18252; MUID:92078153; PMID:1744087
A:Accession: S18252
A:Molecule type: mRNA
A:Residues: 1-3707 <NOO>
A:Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
R:Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogell, G.; Sasaki, M.; Yamada, Y.; Hori
J. Biol. Chem. 263, 16379-16387, 1988
A:Title: Identification of cDNA clones encoding different domains of the basement membr
A:Reference number: A92680; MUID:89034110; PMID:2972708
A:Accession: A31917
A:Molecule type: mRNA
A:Residues: 940-1601 <NO2>
A:Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A:Accession: B31917
A:Molecule type: mRNA
A:Residues: 1870-2600 <NO3>
A:Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R:Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A:Title: Structural properties of recombinant domain III-3 of perlecan containing a glo
A:Reference number: S66460; MUID:95377282; PMID:7649154
A:Accession: S66460
A:Molecule type: protein
A:Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C:Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G rep
C:Keywords: glycoprotein
P:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
P:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
P:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
P:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
P:764-811/Domain: laminin-type EGF-like homology <LEG>
P:1159-1206/Domain: laminin-type EGF-like homology <LEG7>
P:1563-1610/Domain: laminin-type EGF-like homology <EG7>
P:1613-1668/Domain: laminin-type EGF-like homology <LEG8>
P:3163-3198/Domain: EGF homology <EGF>
P:3270-3423/Domain: laminin G repeat homology <LG2>
P:3464-3492/Domain: EGF homology <EGF7>
P:1256,1891,2136,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 10.3%; Score 167.5; DB 2; Length 3707;
Best Local Similarity 26.2%; Pred. No. 6.6e-05;
Matches 55; Conservative 26; Mismatches 68; Indels 61; Gaps 9;
QY 32 VNLKSSNRNPVHBFESVELSCIITHSQTSDPRIEWKK-----IQDQOTVVYFQDN 82
DB 2812 INVTISVHSVVVG--HSEVFECLAGD--PKQVTSKVGHLRPGVQSG----- 2858
QY 83 KIQDGLAGRTDVGKTSIRLWNVTRSDSAIYRCVVALNDRKEVDITIELIVQKVP--- 139
DB 2859 -----TIIRIAHVELADAGYRC--AATNAAGTTQSHVLLVQALPQIS 2900
QY 140 VTPVCRIAPAAVPUGKATLQCBSEGYPRPHYSWYRNDVPLPTDSRANPRFQNSPFHVS 199
DB 2901 TTPPIRVPA-----GSAAVPPQWAS-GYTPPAITWSKVDGDLPPDSRL----- 2942
QY 200 ETGTLVFNVAHKDSDGOYVCIASNDAGAAR 229
DB 2943 ENRMMLPSVRPEDAGTYVCTATNRQGVK 2972

RESULT 12
T29757
Protein UNC-89 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C:Accession: T29757
R:Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid C09D1.
A:Reference number: 220679
A:Accession: T29757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6642 <DUZ>
A:Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CBSP:unc-89
A:Experimental source: strain Bristol N2; clone C09D1
C:Genetics:
A:Gene: CBSP:unc-89
A:Map position: 1
A:Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1; 673; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match 10.3%; Score 167.5; DB 2; Length 6642;
Best Local Similarity 27.1%; Pred. No. 0.00013;
Matches 57; Conservative 30; Mismatches 68; Indels 55; Gaps 9;
QY 45 EFESVELSCIITHSQTSDPRIEWKKIQDQO---TYYVVFQNKIQDLAG 90
DB 3828 EFVELLRSCVTVERKQAILKCKVGEPRPKIKWTK--EKKVEMSGARVRAEHODGTU-- 3883
QY 91 RTDVGKTSIRLWNVTRSDSAIYRC-----VVALNDRKEVDITIELIVQ 136
DB 3884 -----TLTFDNTVQADAGYRCAEYGSAMTEGPIIVTLLEGAPKIDGCEAPDFLQ 3935
QY 137 VKPVPVCRIAPAAVPUGKATLQCBSEGYPRPHYSWYRNDVPLPTDSRANPRFQNSPFH 196
DB 3936 VK-----FAVWVVGETAIVLEGKIS-GKPKPSVKWYKNGEELKPSDRV--KIEN----- 3980
QY 197 VNSGTGLVFNVAHKDSDGOYVCIASNDAG 226
DB 3981 LDDGTQRUTVTNKLDDMDDEYRCASNEFG 4010

RESULT 13
T17346
hypothetical protein DKFp586O1624.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17346
R:Duisterhoft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18727

A:Accession: T17346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-483 <DUZ>
A:Cross-references: EMBL:AL117666
A:Experimental source: adult uterus; clone DKFp586O1624
C:Genetics:
A:Note: DKFp586O1624.1

Query Match 10.2%; Score 166; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 8.1e-06;
Matches 66; Conservative 44; Mismatches 101; Indels 78; Gaps 16;
QY 51 LSCIITHSQTSDPRIEWKKIQDQOTVVYFQNKIQDLAGR-----TDVFKTSIR 101
DB 8 LECAATGCH--PNPQIAWQK--DGGTDFP-----AARERRRGMVMPDDDDVPFITDVK 53
QY 102 IWNVTRSDSAIYRCVVALNDRKEVDITIELIVQKVPVPCRIP---AAPPVCGKTATL 158
DB 54 I-----DDAGVSC--TAQNSAGSISANATITVLE---TSLVVPLEDRVVSUGETVAL 102
QY 159 QCQSEGYPRPHYSWYRNDVPLPTDSRANPRFQNSPFHVNSETGTLVFNVAHKDSDGOY 218
DB 103 QC-KATGNPPPRITWPKGDRPLSLTER-----HHLTPDNQLLVQNVVAEDAGRYT 152
QY 219 CIASNDAGAARCEQDMVEVDLNIAGIIG-----GVLVVLIVLAVI---TMGICCA 267
DB 153 CEMNTLGTSTRAHSQ-----LSVLPAAGCKRGKGTGIFTIAVSSIVLTSLVWVCIIY 206
QY 268 RRGCFISSKQDGSYKSPGKHGIV-----NVIRTSREGDFRHKSSFVI 310
DB 207 Q-----TRKSEYSYVNTDETVPVPPDPSYL--SSQGTLSDRQETVV 247

RESULT 14
T33433
hypothetical protein T17A3.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33433
R:Clarke, K.; Rohlfing, T.; Morris, M.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of C. elegans cosmid T17A3.
A:Reference number: 221343
A:Accession: T33433
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-352 <CLA>
A:Cross-references: EMBL:AF078787; PIDN:AAC26956.1; GSPDB:GN00021; CBSP:T17A3.10
A:Experimental source: strain Bristol N2; clone T17A3
C:Genetics:
A:Gene: CBSP:T17A3.10
A:Map position: 3
A:Introns: 21/3; 112/3; 195/2; 341/2

Query Match 10.1%; Score 164.5; DB 2; Length 352;
Best Local Similarity 22.8%; Pred. No. 7.4e-06;
Matches 61; Conservative 57; Mismatches 65; Indels 85; Gaps 17;
QY 43 VHEFESVELSCIITHSQTSDPRIEWK---KIQDQOTVVYFQNKIQDLAGRTDVGKTS 99
DB 143 VYEQDTVNLPCAIPHS-----AINWKSWSRLSNSNT-----SDLSTVTLIDGNSK 188
QY 100 LRIM---NVTRSDSAIYRCVVA---LNRKVEVDITIELIVQKVPV-----PVCRIAPAAV 150
DB 189 YHVTTVKNIK--SGVYTCVTEADFKERRQL---LETVIKVKPASTRPBPKSKMAI 242
QY 151 PVGKTA---TLQCQSEGYPRPHYSWYRNDVPLPTDSRANPRFQNSPFHVNSETGTLVFN 207
DB 243 PNCKSSIBIRIQCNIT-GHPLPEYSWVYDE-----SSGSTLTITS 280
QY 208 AVHKDSDGOYVCIASNDAGAARCEQDMVEVDLNIAG-----TIGGVLVVLIVLAVITMGI 263

Db 281 ----EDSGVFQCIDSKN-----RYVEVNTGSHRKALGFYIIIVALLMSV-TVGV 324
QY 264 CCAYRGCPISSKQ--DGESYKSPGKH 289
Db 325 C-----VFLISERVANGTEKRPVQYN 346

Search completed: June 15, 2004, 11:05:46
Job time : 16 secs

RESULT 15

IJBONC

neural cell adhesion molecule short domain form precursor - bovine

N:Alternate names: NCAM-140
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999
C:Accession: A32976; A38778; B44290; S05402
R:lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki
FEBS Lett. 254, 69-73, 1989
A:Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and
A:Reference number: A32976; MUID:89378239; PMID:2776887

A:Accession: A32976

A:Molecule type: mRNA

A:Residues: 1-853 <LIP>

A:Cross-references: GB:X16451; NID:g60; PIDN:CAA34470.1; PID:g61

A:Accession: A38778

A:Molecule type: protein

A:Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;
A>Note: the authors identified this protein as calmodulin-independent adenylate cyclase

J. Biol. Chem. 261, 3396-3401, 1986

A:Title: Structural and immunological characterization of the amino-terminal domain of n

A:Reference number: A44290; MUID:86140120; PMID:3512556

A:Accession: B44290

A:Molecule type: protein

A:Residues: 20-36 <ROU>

A>Note: 23-Glu was also found

C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C:Comment: Various forms of NCAM are produced by alternative splicing.
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-853/Product: neural cell adhesion molecule, short domain form #status experimental

F:20-719/Domain: extracellular #status predicted <EXT>

F:34-98/Domain: immunoglobulin homology <IMM1>

F:132-191/Domain: immunoglobulin homology <IMM2>

F:152-156/Region: heparin binding #status predicted

F:161-165/Region: heparin binding #status predicted

F:228-288/Domain: immunoglobulin homology <IMM3>

F:261-270/Region: NCAM binding #status predicted

F:321-396/Domain: immunoglobulin homology <IMM4>

F:428-490/Domain: immunoglobulin homology <IMM5>

F:527-604/Domain: fibronectin type III repeat homology <FN3A>

F:633-693/Domain: fibronectin type III repeat homology <FN3B>

F:720-737/Domain: transmembrane #status predicted <TM>

F:738-853/Domain: intracellular #status predicted <INT>

F:41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted

F:222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 164.5; DB 1; Length 853;

Best Local Similarity 25.5%; Pred. No. 2.1e-05;

Matches 59; Conservative 42; Mismatches 85; Indels 45; Gaps 12;

QY 27 CMIEA-----VNLKSNR-----NPVVHPEPSVELSLIITHSQTS-DPRIEWKKIQ 71

Db 96 CVVTABDGTSEATNVNFKIFQKLMFNAPTPQSFREGEDAVIVCDVVSLLPPTIILWK--H 153

QY 72 DGQTTVVYFDNKIOGLAGRTDVFGRKTSIRIMWVTRSDSAIYRCB--VVALNDRKEVDEI 129

Db 154 KGR-----DVILKKDV--RPVLTNNYLGIRIKITDEGTYRCGRILA---RGEINPK 202

QY 130 TIELIVQVKEPVPVCR--IPAAVPVCKTATLQCSSEGGYPRPHYSWYRNDVPLPTDSRAN 187

Db 203 DIQVIVNPPTVQARQIVNATANLQSVTLVC-NAEGFPPTVSWTKDGEQIENE---- 257

QY 188 PRFQNSSFHVNSTGTGLVFNVAHVHDDSGQYCIASNDAGNARCEGQDMEVY 238

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 10:51:49 ; Search time 10 Seconds
(without alignments)
1614.175 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYLPHFL.....VNVTSEGDFFRKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	505	30.9	298	1	JAM2 HUMAN
2	449.5	27.5	300	1	JAM1_MOUSE
3	415	25.4	299	1	JAM1_HUMAN
4	409.5	25.1	298	1	JAM1_BOVIN
5	242.5	14.8	319	1	A33 HUMAN
6	180	11.0	1088	1	NCA1_XENLA
7	178	10.9	1051	1	PTK7_CHICK
8	177	10.8	333	1	AMAL_DROME
9	172.5	10.6	365	1	CMAR_HUMAN
10	172.5	10.6	837	1	NCM2_MOUSE
11	172.5	10.6	858	1	NCA1 RAT
12	170	10.4	349	1	LACH_SCHAM
13	169.5	10.4	725	1	NCA2_MOUSE
14	169.5	10.4	1115	1	NCA1_MOUSE
15	169	10.3	1092	1	NCA2_XENLA
16	167.5	10.3	837	1	NCA2 HUMAN
17	167.5	10.3	3707	1	PCBM_MOUSE
18	167.5	10.3	6632	1	UN89_CAEEL
19	164.5	10.1	853	1	NCA1_BOVIN
20	163	10.0	344	1	NTRI HUMAN
21	163	10.0	761	1	NCA2 HUMAN
22	163	10.0	848	1	NCA1 HUMAN
23	161	9.9	1377	1	NEOL RAT
24	159.5	9.8	1277	1	CAML_FUGRU
25	159	9.7	1091	1	NCA1_CHICK
26	157	9.6	344	1	NTRI_MOUSE
27	156	9.6	344	1	NTRI RAT
28	156	9.6	1493	1	NB01_MOUSE
29	155	9.5	353	1	CFPU_CHICK
30	151.5	9.3	365	1	CMAR_MOUSE
31	151.5	9.3	873	1	FAS2_DROME
32	151	9.2	1912	1	PTPD HUMAN
33	150	9.2	1694	1	SN_MOUSE
34	149.5	9.2	4391	1	PCBM HUMAN
35	148.5	9.1	1070	1	PTK7_HUMAN
36	148.5	9.1	1461	1	NEOL_HUMAN
37	148	9.1	1040	1	AXO1_HUMAN
38	148	9.1	1040	1	AXO1 RAT
39	147.5	9.0	847	1	CD22 HUMAN
40	145	8.9	359	1	LACH_DROME
41	144.5	8.8	702	1	CEAS_HUMAN
42	144	8.8	521	1	CEAL_MOUSE
43	143.5	8.8	1443	1	NEOL_CHICK
44	143	8.8	345	1	OPCM_BOVIN
45	143	8.8	345	1	OPCM_RAT

ALIGNMENTS

RESULT 1				
JAM2_HUMAN				
ID	JAM2_HUMAN	STANDARD;	PRT;	298 AA.
AC	P57087;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DB	Junctional adhesion molecule 2 precursor (Vascular endothelial			
DB	Junction-associated molecule) (VE-JAM).			
GN	JAM2 OR VEJAM OR C21ORP43.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Vascular endothelial cells;			
RX	MEDLINE=20317114; PubMed=10779521;			
RA	Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.,			
RT	"Vascular endothelial junction-associated molecule, a novel member of			
RT	the immunoglobulin superfamily, is localized to intercellular			
RL	J. Biol. Chem. 275:19139-19145(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=20507930; PubMed=10945976;			
RA	Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkce R.J.,			
RA	Vanderlicke P., Morris A.P., Brock T.A.;			
RT	"A novel protein with homology to the junctional adhesion molecule:			
RT	Characterization of leukocyte interactions."			
RL	J. Biol. Chem. 275:34750-34756(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Joquehall N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

DR GO: GO:0005515; P:protein binding; IPI.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IGv: 1.
DR PROSITE: PSS0835; IG-LIKE; 2.
KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
Repeat; Signal; 3D-structure.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
FT DOMAIN 27 238 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 239 259 POTENTIAL.
FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 122 IG-LIKE V-TYPE 1.
FT DOMAIN 134 230 IG-LIKE V-TYPE 2.
FT DISULFID 49 108 POTENTIAL.
FT DISULFID 152 212 POTENTIAL.
FT CARBOHYD 42 42 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 300 AA; 32368 MM; 391F3E48FF3B97EC CRC64;

Query Match 27.5%; Score 449.5; DB 1; Length 300;
Best Local Similarity 34.2%; Pred. No. 5.2e-11;
Matches 102; Conservative 64; Mismatches 117; Indels 15; Gaps 7;

QY 20 LLLPFGCMIEAV-----NLKSNRPVPHVEFVELSCIIITHSQSPRIEKKIQDQG 74
DB 11 LLLPFTSMILSLVQKGSVYTAQSDVQVPEHSIKLTC--TVSGFSSPRVKKFVQGST 68
QY 75 TTYVYFDNKIQGLAGRTDVFQKTSRLRWVTSDSNRYCEVALNDKREVDIEIILI 134
DB 69 TALVCYNSQITAPYADRVT--TFSSGTFSSVTRKNGEYTC--MVSEGGQNGYGEVSIHLT 126
QY 135 VQVKPTVPCRIPAAYVGVGTATLQOESGYPHPHYMYRNDVPLPT--DSRANPRFONS 193
DB 127 VLVPSPKPTISVPSSVTIGNRAVLTCSEHDSPPSEYFWFKDGISMLTADAKKTRAFMNS 186
QY 194 SPVNSSETGLVFNVAHKDQSGYQYCIANSAGAA--RCEQDMVEVDLNTAGIIGVLVV 252
DB 187 SPTIDPKSGDLIPDVTAFDSGEYVCOAQNCGYGTAMRSEAAHMDAVELNMGVIAAFLVT 246
QY 253 LIVLAVITWICCAVRCGCPFISSKDGESYKSKGHDGVNYIETSEGGPRKHSSTVI 310
DB 247 LILLGLLIFGWFPAYSRGYPETTKG-----TAPGKKVIYSQPSRSEGEFKQTSFLV 300

RESULT 3
JAM1_HUMAN STANDARD; PRT; 299 AA.
AC Q9Y624;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Juncional adhesion molecule 1 precursor (JAM) (Platelet adhesion
DE molecule 1) (PAM-1) (Platelet FII receptor) (UNQ264/PRO301).
GN FIIIR OR JAM1 OR JCAM.
OS Homo sapiens (Human).
OC Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RX [1]
SQ SEQUENCE FROM N.A.
RP MEDLINE=99323940; PubMed=10395639;
RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.;
RT "Combined treatment of TGF-alpha and IFN-gamma causes redistribution
RT of junctional adhesion molecule in human endothelial cells.";
RL J. Immunol. 163:553-557(1999).
RN [2]
SQ SEQUENCE FROM N.A.
RP Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
RA Kornecki E.;
RT "Molecular cloning and sequencing of the cDNA of FII receptor, a

novel Ig superfamily member from human platelets.";
Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.
[3]
SQ SEQUENCE FROM N.A.
RP Naik U.P., Naik M.U., DeLeon P., Spychala J.;
RT "Cloning and characterization of PAM-1, a novel platelet adhesion
RT molecule involved in platelet activation.";
Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
[4]
SQ SEQUENCE FROM N.A.
RP MEDLINE=21154917; PubMed=11230166;
RX Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoerge W., Bloeker H., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435(2001).
[5]
SQ SEQUENCE FROM N.A.
RP MEDLINE=22887296; PubMed=12975309;
RX Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yaneura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
[6]
SQ SEQUENCE FROM N.A.
RP TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Ruben G.M., Schetz T.B.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC [1]
CC -I- FUNCTION: Seems to play a role in epithelial tight junction
CC formation. Appears early in primordial forms of cell junctions and
CC recruits PAR3. The association of the PAR6-PAR3 complex may
CC prevent the interaction of PAR3 with JAM1, thereby preventing
CC tight junction assembly (By similarity). Plays a role in
CC regulating monocyte transmigration involved in integrity of
CC epithelial barrier. Involved in platelet activation.
CC -I- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
CC association between PAR3 and PAR6B probably disrupts this
CC interaction (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.

Db 128 LVPSKPTINVPSSVTIGTRAVLTCSEKDGSPSEYKWFQGVEMPLEPKSNRAPSSSY 187

Qy 196 HVNSETGLVFNVAHKDDSGYYCIASND-AGAACGQDMVEYVDLNIAGIIGVVLVI 254

Db 188 TLNQKTGELIFDPVSASDTGDFTCQAGVSPVKSITVHMDAVELNVGGVIAAVFVTLI 247

Qy 255 VLAVITWGICVAYRGCFISSKQDGS----YKSPRGHGDGVNYRTSEEDPRHKSFPVI 310

Db 248 LGLALIGIMPAYSRYGYPDRAGKTSNKKVIYSP-----NARSDGEPRQTSSFLV 298

RESULT 5

A33_HUMAN

ID A33_HUMAN STANDARD; PRT; 319 AA.

AC Q99795;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Cell surface A33 antigen precursor (Glycoprotein A33).

GN GPA33.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Colon carcinoma;

RX MEDLINE=97165045; PubMed=9012807;

RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,

RA Moritz R.L., Tu G.-P., Ji H., Whitehead R.H., Groenen L.C.,

RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,

RA Burgess A.W.;

RT "The human A33 antigen is a transmembrane glycoprotein and a novel

RT member of the immunoglobulin superfamily.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).

RN [2]

RP POST-TRANSLATIONAL MODIFICATIONS.

RX MEDLINE=9736159; PubMed=9245713;

RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,

RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,

RA Simpson R.J.;

RT "Characterization of posttranslational modifications of human A33

RT antigen, a novel palmitoylated surface glycoprotein of human

RT gastrointestinal epithelium.";

RL Biochem. Biophys. Res. Commun. 236:682-686(1997).

CC -1- FUNCTION: May play a role in cell-cell recognition and signaling.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: Expressed in normal gastrointestinal

CC epithelium and in 95% of colon cancers.

CC -1- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED

CC CARBOHYDRATE.

CC -1- PTM: Palmitoylated.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC

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CC

CC ENBL; U79725; AAC50957.1; -

CC Genew; HGNC:4445; GPA33.

CC MIM; 602171; -

CC GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.

CC GO; GO:0004872; F:receptor activity; TAS.

CC InterPro; IPR007110; Ig-like.

CC InterPro; IPR003596; Ig_v.

CC Pfam; PF00047; Ig; 2.

CC SMART; SM00406; IGV; 1.

CC PROSITE; PSS0835; IG_LIKE; 2.

KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;

KW Transmembrane; Signal; Antigen.

FT SIGNAL 1 21

FT CHAIN 22 319

FT DOMAIN 22 235

FT TRANSMEM 236 256

FT TRANSMEM 257 319

FT DOMAIN 22 134

FT DOMAIN 140 227

FT DOMAIN 258 261

FT DISULFID 43 117

FT DISULFID 146 222

FT DISULFID 162 211

FT CARBOHYD 112 112

FT CARBOHYD 200 200

FT CARBOHYD 223 223

SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAP45C2408E CRC64;

Query Match 14.88; Score 242.5; DB 1; Length 319;

Best Local Similarity 25.78; Pred. No. 2.3e-13;

Matches 80; Conservative 49; Mismatches 123; Indels 59; Gaps 12;

Qy 29 IEAVNLKSSNRNPVHFESVELSCIITHSOTS--DPRIEWKKIQDGGTYVY---PDK 83

Db 19 VDAISVETPDVLRASQSKSVTLPTCY-HTSTSREGLIQWDKLLTHTRVWIWPPSNK 77

Qy 84 --TQDGL-----AGRTDVFQKTSRLIMNVTSDSAIYRCVVALNDRKVEDEITY 131

Db 78 NYIHGELYKNRVSTISNNAEQSD---ASITDQLTMADNGTYECSVLSMDLEGNTKSRV 133

Qy 132 ELIVQVQVTPVCPRIPAAPVPGTKATLQCOBSESGYPRPHYSWYRNDV-----PLPTDSRA 186

Db 134 RLVLVPPSPCEGIBEGTIIQNNIQTCSKESPTPQYSWKRYNINLQOPLAQPASG 193

Qy 187 NPFQNSPHVNSGTGLVFNVAHKDDSGYYCIASNDAG-----AARCEGQDMVEY 238

Db 194 QP-----VSLKNISTDTSGYICTSSNEEGTPCNIITVAVRSPSNVALY 238

Qy 239 DLMIAHIGLVVLVILVAVITWGICVAYRGCFISSKQDGS-----ESYKSPRGHGDGVNYI 294

Db 239 ----VGLAVGVAAALIIIGII-IVCCCRGKDDNTEDKEDARPNNREAYEPEPEQLRELSR 293

Qy 295 RTSEEGDFRHK 305

Db 294 ERREEDDYRQ 304

RESULT 6

NCAL_XENLA

ID NCAL_XENLA STANDARD; PRT; 1088 AA.

AC P16170;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM

DE 180).

DE NCAM1.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A. (ISOPFORMS N-CAM 140 AND N-CAM 180).

RX MEDLINE=90098871; PubMed=2481269;

RA Krieg P.A., Sakaguchi D.S., Kintner C.R.;

RT "Primary structure and developmental expression of a large

RT cytoplasmic domain form of Xenopus laevis neural cell adhesion

RT molecule (NCAM).";

RL Nucleic Acids Res. 17:10321-10335(1989).

CC -1- FUNCTION: This protein is a cell adhesion molecule involved in

CC neuron-neuron adhesion, neurite fasciculation, outgrowth of

CC neurites, etc.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 KW Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;
 KW Immunoglobulin domain; Repeat.

FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 1051 TYROSINE-PROTEIN KINASE-LIKE 7.
 FT DOMAIN 23 685 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 686 706 POTENTIAL.
 FT DOMAIN 707 1051 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 23 105 IG-LIKE C2-TYPE 1.
 FT DOMAIN 115 204 IG-LIKE C2-TYPE 2.
 FT DOMAIN 213 298 IG-LIKE C2-TYPE 3.
 FT DOMAIN 308 388 IG-LIKE C2-TYPE 4.
 FT DOMAIN 393 472 IG-LIKE C2-TYPE 5.
 FT DOMAIN 487 566 IG-LIKE C2-TYPE 6.
 FT DOMAIN 573 661 IG-LIKE C2-TYPE 7.
 FT DOMAIN 777 1048 PROTEIN KINASE; INACTIVE.
 FT DISULFID 40 88 BY SIMILARITY.
 FT DISULFID 137 187 BY SIMILARITY.
 FT DISULFID 234 282 BY SIMILARITY.
 FT DISULFID 326 372 BY SIMILARITY.
 FT DISULFID 414 462 BY SIMILARITY.
 FT DISULFID 505 551 BY SIMILARITY.
 FT DISULFID 594 645 BY SIMILARITY.
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 264 264 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 548 548 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 1051 AA; 116366 MW; 1752442AER4CB702 CRC64;

Query Match 10.9%; Score 178; DB 1; Length 1051;
 Best Local Similarity 28.3%; Pred. No. 3.2e-07;
 Matches 72; Conservative 29; Mismatches 109; Indels 44; Gaps 12;

QY 45 EP-ESVELSCITHSOTSPRIEWKIQDQQTYYVVDNKGIDLAGRTDVPKTSLRW 103
 DB 496 EFNKEVTVSCATGRE--RPTQWTK--TDG-----SSLSHSHVSHRAGI-----LSFH 539
 QY 104 NTRSDSALYRCVVALNDKVEDEITIELIVQKVPFVPCRPAAVPGKATLQOQS 163
 DB 540 KVSRSDSGNMTC--IASNSPQSEIRATVOLVAVVTFKLEPEPTTYQGHATMPCQ-A 596
 QY 164 EGVPRPHYSWYNDVPLPTDSRANPRFQNSFHVNSSETGLFVNAVHKDDSGOYYCIASN 223
 DB 597 EGDVPVHIQKQKDKIL-DPSKLLPRIQ-----IMPNGSLVIYDVTTEDSGKYTCIAGN 649
 QY 224 DA-----GAARCEGQDMEV-YD-LNIAGIIGGVVLVVLVAVITMGICCA 266
 DB 650 SCNIXHREAFVVDKPAAEDEGPPSHPTPKMIQTIGLSVGAAYVAVIIVLGLMFPYCK 709
 QY 267 YRGCFPISSKQDGE 280
 DB 710 RRKAKELKKHPEGE 723

RESULT 8

ANAL_DROME STANDARD; PRT; 333 AA.
 AC P15364; Q9V3A5;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amalgam protein precursor.
 GN AMA OR BG:DS00276.6 OR CG2198.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Oregon-R;
 RX MEDLINE=89028670; PubMed=3141062;
 RA Seeger M.A., Haffley L., Kaufman T.C.;
 RT "Characterization of amalgam: a member of the immunoglobulin
 RL superfamily from Drosophila."; Cell 55:589-600(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
 RA Palazzolo M.J.;
 RT "Complete sequence of the Antennapedia complex of Drosophila";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.A.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriel J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
 RA Borokova D., Botchan M.R., Bouck B.J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Maya A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flesher C., Gabrielian A.B., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley; TISSUE=Embryo;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource."; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 RL -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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DR EMBL: AF169363; AAF05908.1; JOINED.
DR EMBL: AF169364; AAF05908.1; JOINED.
DR EMBL: AF169365; AAF05908.1; JOINED.
DR EMBL: AF200465; AAF24344.1; -.
DR EMBL: AF242865; AAG01088.1; -.
DR EMBL: AF242862; AAG01088.1; JOINED.
DR EMBL: AF242864; AAG01088.1; JOINED.
DR EMBL: BC003684; AAOH03684.1; -.
DR EMBL: BC010536; AAH10536.1; -.
DR PDB: 1E4J; 13-JUL-01.
DR PDB: 1FSW; 08-NOV-99.
DR PDB: 1KAC; 24-NOV-99.
DR Genew; HGNC:2559; CXADR.
DR MIM; 602621; -.
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:004872; F: receptor activity; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT TRANSMEM 238 258
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT BY SIMILARITY.
FT DISULFID 41 128
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FB64 CRC64;

Query Match 10.6%; Score 172.5; DB 1; Length 365;
Best Local Similarity 25.9%; Pred. No. 2.5e-07;
Matches 68; Conservative 38; Mismatches 116; Indels 41; Gaps 11;

QY 47 ESYELSLCIITHS-QTSDP-RIEW-----KKIQDQGVTVVYVDNKKIQG----DLAQRD 93
DB 35 ETAYLPCKFTLSPEQDQPLDIEMWLSPADNQKVD--QVILYSGDKLYDDYDPLKGRVH 92
QY 94 V-----FGKTSLRINWVTSLSAIVRCVVALNDRKVEDITELIVQVYPTVPCRI 147
DB 93 FTSNDLKGSDASINVTNLQSLDGTQCKV---KKAPGVANKKHLVVLVKPSGARCYVD 149
QY 148 AAVPVGKTATLQCESEGYRPHYSWYRNDVPLPTDSRANPRQNSGFHYNSGTGLVFN 207
DB 150 GSEEGISGDFKIRCEPKGSLPLQYEWOK-----LSDSQKMP-----TSWLAEMTSSVISVK 200
QY 208 AVHKDQSGQYYCIASNDAGAACBQDMVEVDLNIAGIIGGVLV-VLIVLAVITMGICCA 266
DB 201 NASSEYSGTYSCTVRNVRGSDQCLRLNVTVPSPKAGLIAGIIGTLLALIGLIIFCC 260
QY 267 YRRCGCTISSQDGEYSKPSKQHD 289
DB 261 RK-----KREKREYKEVHH 276

RESULT 10
NCM2 MOUSE
ID NCM2 MOUSE STANDARD; PRT; 837 AA.
AC Q35136; Q35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/C; TISSUE=Olfactory neuroepithelium;
RX MEDLINE=97368238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family
RT related to zone-to-zone projection of olfactory and vomeronasal
RT axons.";
RL J. Neurosci. 17:5830-5842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene
RT with a potential role in selective axonal projection.";
RL J. Biol. Chem. 272:26083-26086(1997).
CC -|- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC attached to the membrane by a GPI-anchor (short isoform).
CC -|- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O35136-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O35136-2; Sequence=VSP_002590;
CC -|- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
CC vomeronasal neurons in a zone-specific manner.
CC -|- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -|- SIMILARITY: Contains 2 fibronectin type III domains.
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF001287; AAB69125.1; -.
CC EMBL; AF001286; AAB69124.1; -.
CC EMBL; AF016619; AAC53375.1; -.
CC MGD; MGI:97282; Ncam2.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00047; Ig; 5.
CC SMART; SM00060; FN3; 2.
CC PROSITE; PS0835; IG_LIKE; 5.
CC Cell adhesion; Transmembrane; Glycoprotein; Repeat;
CC Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
CC SIGNAL 1 19
CC CHAIN 20 837
CC DOMAIN 20 697
CC TRANSMEM 698 718
CC DOMAIN 719 837
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC IG-LIKE C2-TYPE 1.
CC IG-LIKE C2-TYPE 2.
CC IG-LIKE C2-TYPE 3.
CC IG-LIKE C2-TYPE 4.
CC IG-LIKE C2-TYPE 5.
CC IG-LIKE C2-TYPE III 1.
CC FIBRONECTIN TYPE-III 2.
CC PROBABLE.
CC DISULFID 42 93
CC DISULFID 136 186
CC DISULFID 232 281

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FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 694 837 ITRMCKGSSGSSKSLERGLKAAVILVTVDSGFFIRQCGLLMC
FT DERLTHEDGSPVNEPTPLTERPEKLPKKEGKEVLNA
FT ETBIKVSNDIIQSKEDDIKA -> NCCEANKENGQSQSH
FT LNAVGFVFIWMSLCLF (in isoform Short).
FT /FTID=VSP_002590.
SQ SEQUENCE 837 AA; 93203 MW; 70473B053A2D65A5 CRC64;

Query Match 10.6%; Score 172.5; DB 1; Length 837;
Best Local Similarity 30.1%; Pred. No. 7e-07;
Matches 55; Conservative 26; Mismatches 75; Indels 27; Gaps 8;

QY 47 ESVELSCIITHSQTSDPRIEMKIQDQTTVVYFDNKIQGLAGRTDVFQKTSIRIWNVT 106
DB 130 EDAEVCVSSSPA--FAVSW-----LYNEEVTTIPDRFAVANNULQILNIN 177
QY 107 RSDSAIYRCVEVALNDRKVEDEITELIVQKVP--VTPVCRIPAAPVPVGTATLQOQSE 164
DB 178 KSDBGIVRCB--GRVEARGEIDFRDIIVIVNPPAIMMPQKSFNATARGEBMTLTCKAS- 235
QY 165 GYRPHYSWYRNDVPLPTDSRANRPNSSPHV-NSETGTLVFNVAHKDSDGGVYCIASN 223
DB 236 GSPDFTISWFRNGKLIB-----ENEKILKSGNTELTVRNLIINK-DOGSIVCKATN 285
QY 224 DAG 226
DB 286 KAG 288

RESULT 11
NCAL_RAT STANDARD; PRT; 858 AA.
AC P13596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=86053265; PubMed=3680385;
RA Small S.J., Shull G.E., Santoni M.-J., Akesson R.;
RT "Identification of a cDNA clone that contains the complete coding
sequence for a 140-kD rat NCAM polypeptide.";
RL J. Cell Biol. 105:2335-2345(1987).
[2]
RP SEQUENCE OF 355-364 FROM N.A.
RX MEDLINE=90166485; PubMed=2483093;
RA Small S.J., Haines S.L., Akesson R.A.;
RT "Polypeptide variation in an N-CAM extracellular immunoglobulin-like
fold is developmentally regulated through alternative splicing.";
RL Neuron 1:1007-1017(1988).
CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC neurites, etc.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:

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CC Event-Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P13596-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; X06564; CAA29809.1; -;
CC EMBL; M32611; AAA41679.1; -;
CC PIR; S00846; IURTNC.
CC PDB; 1BPF; 27-OCT-00.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00047; ig; 5.
CC SMART; SM00060; FN3; 2.
CC SMART; SM00408; IGC2; 5.
CC PROSITE; PSS0835; IG_LIKE; 5.
CC Cell adhesion; Glycoprotein; Transmembrane; Repeat;
CC Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
CC 3D-structure.
CC SIGNAL 1 19 NEURAL CELL ADHESION MOLECULE 1, 140 kDa
CC CHAIN 20 858 ISOFORM.
CC DOMAIN 20 721 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 722 739 POTENTIAL.
CC DOMAIN 740 858 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 20 111 IG-LIKE C2-TYPE 1.
CC FT DOMAIN 116 205 IG-LIKE C2-TYPE 2.
CC FT DOMAIN 212 302 IG-LIKE C2-TYPE 3.
CC FT DOMAIN 309 414 IG-LIKE C2-TYPE 4.
CC FT DOMAIN 417 502 IG-LIKE C2-TYPE 5.
CC FT DOMAIN 514 615 FIBRONECTIN TYPE-III 1.
CC FT DOMAIN 616 712 FIBRONECTIN TYPE-III 2.
CC FT DOMAIN 152 156 HEPARIN-BINDING (POTENTIAL).
CC FT DOMAIN 161 165 HEPARIN-BINDING (POTENTIAL).
CC FT DISULFID 41 96 BY SIMILARITY.
CC FT DISULFID 139 189 BY SIMILARITY.
CC FT DISULFID 235 288 BY SIMILARITY.
CC FT DISULFID 330 396 BY SIMILARITY.
CC FT DISULFID 437 490 BY SIMILARITY.
CC FT CARBOHYD 222 222 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 316 316 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 348 348 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 434 434 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 489 489 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 858 AA; 94658 MW; EALA064EA0550F6 CRC64;

Query Match 10.6%; Score 172.5; DB 1; Length 858;
Best Local Similarity 27.1%; Pred. No. 7.2e-07;
Matches 61; Conservative 43; Mismatches 84; Indels 37; Gaps 13;

QY 26 GCMIEA-VNLIKSNR-----NPVVHFESEVELSCIIHESQTS-DPRIEMKIQDQTTVV 78
DB 103 GTOSEATVNVKIFQKLPKNAFTPQBFKGBDAVIVCDVWSSLPPTIWK--HGR----- 156
QY 79 YFDNKIQGLAGRTDVFQKTSIRIWNVTNVSALYRCB--VVALNDRKVEDEITELIVQ 136
DB 157 --DVILKDV--RFIVLSNLYLQIRKTKDGTGTCRGLA---RGEINFKDIQVIVN 209
QY 137 VKFVTPVCR--IPAAVPVGTATLQOQSESGYRPHYSWYRNDVPLPTDSRANRPNSS 194

```

Db 210 VPFTVQARQSIIVNATNLQSVTLVC-DADGFPEPTMTSKDGEPIENEE-----EDDE 262

QY 195 FFV-NSETGLTVFNAVHKDDSGYCTIASNDAGAACRCEGDMVEY 238

Db 263 KHIFSDSSSELTRNDKDEABYVCIAENKAGE-----QDASIH 302

RESULT 12

LACH SCHAM STANDARD; PRT; 349 AA.

AC Q26474;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB Lachesin precursor.

GN LAC

OS Schistocerca americana (American grasshopper).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.

OX NCBI_TaxID=7009;

RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=94038693; PubMed=8223276;

RA Karlstrom R.O., Wilder L.P., Bastiani M.J.;

RT "Lachesin: an immunoglobulin superfamily protein whose expression correlates with neurogenesis in grasshopper embryos.";

RL Development 118:509-522(1993).

CC -!- FUNCTION: MAY PLAY A ROLE IN EARLY NEURONAL DIFFERENTIATION AND AXON OUTGROWTH.

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- TISSUE SPECIFICITY: EXPRESSED BY ALL NEUROGENIC CELLS EARLY, BUT ONLY THOSE CELLS THAT BECOME NEUROBLASTS CONTINUE TO EXPRESS IT..

CC EXPRESSED BY NEUROBLASTS, GANGLION MOTHER CELLS AND NEURONS EARLY IN THEIR LIVES, BUT EXPRESSION BECOMES RESTRICTED TO A SUBSET OF NEURONS AS DEVELOPMENT PROGRESSES. EXPRESSED BY SENSORY NEURONS AS THEY DELAMINATE FROM THE BODY WALL ECTODERM. IT IS ALSO PRESENT ON GROWING AXONS OF THE CNS AND PNS AND BECOMES RESTRICTED TO A SUBSET OF AXONS LATER IN DEVELOPMENT.

CC -!- DEVELOPMENTAL STAGE: EXPRESSED ON DIFFERENTIATING NEURONAL CELLS FROM THE ONSET OF NEUROGENESIS IN BOTH THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.

CC -!- PTM: The N-terminus is blocked.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -----

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CC -----

DR EMBL; L13256; AAC37185.1; -.

DR HSP; P80362; 1WT1.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00408; Igc2; 2.

DR PROSITE; PS0835; IG LIKE; 3.

KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;

KW Repeat; Signal; Lipoprotein.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 332 LACHESIN.

FT PROPEP 333 349 REMOVED IN MATURE FORM (POTENTIAL).

FT DOMAIN 22 127 IG-LIKE V-TYPE.

FT DOMAIN 132 218 IG-LIKE C2-TYPE 1.

FT DOMAIN 222 315 IG-LIKE C2-TYPE 2.

FT DISULFID 43 110 POTENTIAL.

FT DISULFID 154 201 POTENTIAL.

FT DISULFID 244 299 POTENTIAL.

FT CARBOHYD 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT LIPID 332 GPI-anchor amidated glycine (Potential).

SQ SEQUENCE 349 AA; 38974 MW; 5F139A44BF849689 CRC64;

Query Match 10.4%; Score 170; DB 1; Length 349;

Best Local Similarity 25.3%; Pred. No. 3.8e-07;

Matches 63; Conservative 39; Mismatches 73; Indels 74; Gaps 14;

QY 9 LRLYARLPHFELLPRGCMIRAVNLKSNRNPPVHEFB-----SYELSCIIHQS 59

DB 3 LRLYTFVGFSSVY-----AQTTFISYISQEQIKDGGTVELECSVOYQA 49

QY 60 TSDPRIWKIKIQDQ-----TTYVYFNDKIQDLAGRTDVFQKT-SLRIMNVT 108

DB 50 --DYPVLWMKVDRNRQVDPPISTGSSLIIRDSE---PALRYDTASSTVTLQIKDIET 103

QY 109 DSAIYRCEV-VALNDRKEVDEITIELIVQKPTVPFCRIPA-----AVPVGTATL 158

DB 104 DAGFYQCQVIIGLNK-----ITAEYDLQVR-----RPPVTSNSTRSLVSEGGQAVRL 152

QY 159 QCQEGEGYPRPHYSWYR-NDVPLPTDSRANPRFQNSFHVNSSETGLTFVNAVHKDSSGOY 217

DB 153 ECV-AGGYAPRVSRRNNALPTG-----GSIYRGN-----VLKISRICKEDRGTY 199

QY 218 YCIASNDAG 226

DB 200 YCVAENGVG 208

RESULT 13

NCA2 MOUSE STANDARD; PRT; 725 AA.

ID NCA2 MOUSE STANDARD; PRT; 725 AA.

AC P13594; Q61950;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120) (NCAM-120).

DE NCAM1 OR NCAM.

OS Mus musculus (Mouse).

OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RX MEDLINE=8724624; PubMed=3595563;

RA Barthele D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C., Hirsch M.-R., Pontecilla-Camps J.-C., Goridis C.;

RT "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000 polypeptide without a membrane-spanning region.";

RL EMBO J. 6:907-914(1987).

RN [2]

SEQUENCE OF 20-700 FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=89251563; PubMed=2721486;

RA Santoni M.J., Barthele D., Vopper G., Boned A., Goridis C., Wille M.;

RT "Differential exon usage involving an unusual splicing mechanism generates at least eight types of NCAM cDNA in mouse brain.";

RL EMBO J. 8:385-392(1989).

RN [3]

SEQUENCE OF 642-725 FROM N.A.

RX MEDLINE=88283628; PubMed=3396534;

RA Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;

RT "Differential splicing and alternative polyadenylation generates distinct NCAM transcripts and proteins in the mouse.";

RL EMBO J. 7:625-632(1988).

RN [4]

SEQUENCE OF 20-36.

RX MEDLINE=86140120; PubMed=3512556;

RA Rougon G., Marshak D.R.;

RT "Structural and immunological characterization of the amino-terminal domain of mammalian neural cell adhesion molecules.";

RL J. Biol. Chem. 261:3396-3401(1986).

CC -1- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc.

CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -1- ALTERNATIVE PROTEIN: Contains 2 fibronectin type III domains.

CC Event-Alternative splicing; Named isoforms=3;

CC Name=N-CAM 120;

CC IsoId=PI3594-1; Sequence=Displayed;

CC Name=N-CAM 180;

CC IsoId=PI3595-1; Sequence=External;

CC Name=N-CAM 140;

CC IsoId=PI3595-2; Sequence=External;

CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.

CC -1- SIMILARITY: Contains 2 fibronectin type III domains.

CC -----

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CC or send an email to license@sib-sib.ch.

CC -----

DR EMBL; Y00051; CAA68263.1; -

DR EMBL; X15049; CAA33148.1; ALT_SEQ.

DR EMBL; X07195; CAA30173.1; -

DR PIR; A29673; IJNSNG.

DR PDB; 2NCM; 12-MAR-97.

DR PDB; 3NCM; 23-JUL-99.

DR MGD; MGI:97281; Ncam1.

DR InterPro; IPR008957; FN III-like.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_C2.

DR Pfam; PF00041; fn3; 2.

DR Pfam; PF00047; ig; 5.

DR SMART; SM00060; FN3; 2.

DR SMART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 5.

DR Cell adhesion; Glycoprotein; Repeat; Alternative splicing;

DR Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;

DR 3D-structure. 1 19

FT SIGNAL 20 725

FT CHAIN 1 19

FT DOMAIN 20 111

FT IG-LIKE C2-TYPE 1.

FT IG-LIKE C2-TYPE 2.

FT IG-LIKE C2-TYPE 3.

FT IG-LIKE C2-TYPE 4.

FT IG-LIKE C2-TYPE 5.

FT FIBRONECTIN TYPE-III 1.

FT FIBRONECTIN TYPE-III 2.

FT HEPARIN-BINDING (POTENTIAL).

FT HEPARIN-BINDING (POTENTIAL).

FT PROBABLE.

FT PROBABLE.

FT PROBABLE.

FT PROBABLE.

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT ERSRSVS -> DERHIFSD (IN REF. 2).

FT V -> L (IN REF. 2).

FT QD -> K (IN REF. 2).

FT T -> R (IN REF. 2).

FT D -> V (IN REF. 2).

FT MOPSES -> SAATEP (IN REF. 2).

FT PEL -> REP (IN REF. 2).

FT CONFLICT 600 602

FT CONFLICT 657 657 H -> D (IN REF. 2 AND 3).

SQ SEQUENCE 725 AA; 80296 MW; C2AB8B4461C6B2F CRC64;

Query Match 10.4%; Score 169.5; DB 1; Length 725;

Best Local Similarity 27.7%; Pred. No. 1e-06;

Matches 62; Conservative 43; Mismatches 84; Indels 35; Gaps 13;

QY 26 GCMIEA-VNLKSNR-----NPVVHPFESVELSCIITHSOTS-DPRIENKKIQDQGYTVV 78

DB 103 GTQSEATVNVKIFQKLMFKNAPTQBFKGEADAVICDVVSSLPPTTIWK--HKGR----- 156

QY 79 YFNKIQGLAGRTDVGKTSLRINWVTRSDSALYRCE--VVALNDRKVFDEITIELIVQ 136

DB 157 --DVILKKOV--RPVLSNNYLQIRGIKKTDEGTYRCGRILA---RGEINPKDIQIVN 209

QY 137 VKEDVTPVCR--IPAAVPGVKATLQOESSEGYPRPHYSWYRNDVPLPTDSRANPRFQNS 194

DB 210 VPTVQARQSIVNATNLGQSVTLVC-DADGPPTMTKQGEPIENBEE-DRSRSSV 267

QY 195 FHYNSGTGLVFNVAHVHDKDSGYCYCIASNDAGAACRCQDMEVY 238

DB 268 ---SDSSEVTIRNVDKNDREARYVCIENKAGE-----QDASIH 302

RESULT 14

NCAM_MOUSE

ID NCAM_MOUSE STANDARD; PRT; 1115 AA.

AC PI3595; Q61949;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)

DE (NCAM-180).

GN NCAM1 OR NCAM.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RC SEQUENCE FROM N.A. (ISOFORM N-CAM 180).

RC STRAIN=C57BL/6;

RX MEDLINE=87246524; PubMed=3595563;

RA Barthels D., Santoni M.J., Wille W., Ruppert C., Chalk J.C.,

RA Hirsch M.R., Pontecilla-Camps J.C., Goridis C.,

RT "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000 polypeptide without a membrane-spanning region.";

RL EMBL J. 6:907-914(1987).

RN [2]

RC SEQUENCE OF 529-1115 FROM N.A. (ISOFORM N-CAM 140).

RC STRAIN=C57BL/6;

RX MEDLINE=88057687; PubMed=3684567;

RA Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M.,

RA Goridis C., Wille W.;

RT "Analysis of cDNA clones that code for the transmembrane forms of the mouse neural cell adhesion molecule (NCAM) and are generated by alternative RNA splicing.";

RL Nucleic Acids Res. 15:8621-8641(1987).

RN [3]

RC SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).

RX MEDLINE=88283628; PubMed=3396534;

RA Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;

RT "Differential splicing and alternative polyadenylation generates distinct NCAM transcripts and proteins in the mouse.";

RL EMBL J. 7:625-632(1988).

RN [4]

RC SEQUENCE OF 804-1081 FROM N.A. (ISOFORM N-CAM 180).

RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=88247737; PubMed=2454455;

RA Barthels D., Vopper G., Wille W.;

RT "NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse, is encoded by an alternatively spliced transcript.";

RL Nucleic Acids Res. 16:4217-4225(1988).

RN [5]

SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).
 STRAIN=C57BL/6; TISSUE=Brain;
 MEDLINE=89251563; PubMed=2721486;
 Santoni M.J., Barthele D., Vopper G., Boned A., Goridis C., Wille M.;
 "Differential exon usage involving an unusual splicing mechanism
 generates at least eight types of NCAM CDNA in mouse brain.";
 EMBO J. 8:385-392(1989).
 [6]
 SEQUENCE OF 20-36.
 MEDLINE=86140120; PubMed=3512556;
 Rougon G., Marshak D.R.;
 "Structural and immunological characterization of the amino-terminal
 domain of mammalian neural cell adhesion molecules.";
 J. Biol. Chem. 261:3396-3401(1986).
 CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
 neuron-neuron adhesion, neurite fasciculation, outgrowth of
 neurites, etc.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=N-CAM 180;
 CC IsoId=P13595-1; Sequence=Displayed;
 CC Name=N-CAM 140;
 CC IsoId=P13595-2; Sequence=VSP_002588;
 CC Name=N-CAM 120;
 CC IsoId=P13594-1; Sequence=External;
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X07200; CAA30177.1; -;
 DR EMBL; Y00051; -; NOT ANNOTATED_CDS.
 DR EMBL; X6328; CAA29641.1; -;
 DR EMBL; X07195; CAA30173.1; -;
 DR EMBL; X07244; CAA30230.1; -;
 DR EMBL; X15051; CAA33150.1; -;
 DR EMBL; X15052; CAA33151.1; -;
 DR PIR; A29673; IJMSNL.
 DR MGI; 97281; Ncam1.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00408; IGC2; 5.
 DR PROSITE; PS00835; IG_LIKE; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
 FT SIGNAL 1 19
 FT CHAIN 20 1115
 FT DOMAIN 20 711
 FT TRANSMEM 712 729
 FT DOMAIN 730 1115
 FT DOMAIN 20 111
 FT IG-LIKE C2-TYPE 1.
 FT IG-LIKE C2-TYPE 2.
 FT IG-LIKE C2-TYPE 3.
 FT IG-LIKE C2-TYPE 4.
 FT IG-LIKE C2-TYPE 5.
 FT FIBRONECTIN TYPE-III 1.
 FT FIBRONECTIN TYPE-III 2.
 FT HEPARIN-BINDING (POTENTIAL).
 FT HEPARIN-BINDING (POTENTIAL).
 FT PROBABLE. 41 96

FT DISULFID 139 189 PROBABLE.
 FT DISULFID 235 288 PROBABLE.
 FT DISULFID 330 386 PROBABLE.
 FT DISULFID 427 480 PROBABLE.
 FT CARBOHYD 222 222 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 424 424 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 479 479 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 810 1076 Missing (in isoform N-CAM 140).
 FT SEQUENCE 1115 AA; 119351 MW; 2C93DCD474CFBCAF CRC64;
 SQ
 Query Match 10.4%; Score 169.5; DB 1; Length 1115;
 Best Local Similarity 27.7%; Pred. No. 1.8e-06;
 Matches 62; Conservative 43; Mismatches 84; Indels 35; Gaps 13;
 QY 26 GCMIEA-VNLKSSNR-----NPVVHEPESVELSCIIHSHOTS-DPRIEWKKIQDQTTVV 78
 DB 103 GTQSEATVNVKIPQKLFKNAPTPOEFKEGEDAVIVCDVVSSLPPTLWK--HKGR---- 156
 QY 79 YFDNKIQGLAGRTDVGKTSLRINVTSDSAIYRCE--VVALNDKREVDDEITIELIVQ 136
 DB 157 --DVILKKOV--RPVLSNNYLQIRGIKTDGTYRCGRILA---RGEINFKDIQIVN 209
 QY 137 VKPVTVPVCR--IPAAVPGVGTATLQOESGYPHPYSWYRNDVPLPTDSRANPRPNSS 194
 DB 210 VPPTQARQSVNATNLQSGVTLVC-DADGFPPTMSWTKGEPPIENHEB-DEKRSRSV 267
 QY 195 FHVNSGTGLVFNVAHKDQGVYCIASNDAGAACRCQDMVEV 238
 DB 268 ----SDSSEVTIRVNDKDEAEVVCIAENKAGE-----QDASIH 302
 RESULT 15
 NCA2 XENLA STANDARD; PRT; 1092 AA.
 ID NCA2 XENLA
 AC P36335;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
 180).
 GN NCAM2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93273239; PubMed=7684721;
 RX Tonissen K.F., Krieg P.A.;
 RT "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus
 laevis are expressed during development and in adult tissues.";
 RL Gene 127:243-247(1993).
 CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
 neuron-neuron adhesion, neurite fasciculation, outgrowth of
 neurites, etc.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;
 CC IsoId=P36335-1; Sequence=Displayed;
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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```
CC -----
CC EMBL; M76710; AAA49910.1; -.
CC PIR; JN0635; JN0635.
CC HSP; P56276; IYTK.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; IG LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
PT SIGNAL 1 19
PT CHAIN 20 1092
FT NEURAL CELL ADHESION MOLECULE 2, 180 kDa
FT ISOFORM.
FT DOMAIN 20 705
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 706 723
FT DOMAIN 724 1092
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 108
FT IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202
FT IG-LIKE C2-TYPE 2.
FT DOMAIN 208 295
FT IG-LIKE C2-TYPE 3.
FT DOMAIN 303 397
FT IG-LIKE C2-TYPE 4.
FT DOMAIN 400 489
FT IG-LIKE C2-TYPE 5.
FT DOMAIN 512 589
FT FIBRONECTIN TYPE-III 1.
FT DOMAIN 618 686
FT FIBRONECTIN TYPE-III 2.
FT DOMAIN 149 153
FT HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 158 162
FT HEPARIN-BINDING (POTENTIAL).
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
SQ SEQUENCE 1092 AA; 118082 MW; CD236BE0EF87AD1 CRC64;

Query Match 10.3%; Score 169; DB 1; Length 1092;
Best Local Similarity 28.4%; Pred. No. 1.9e-06;
Matches 59; Conservative 33; Mismatches 82; Indels 34; Gaps 11;

Qy 32 VNLKSSNR-----NPVVHEFESVELSCIITHSOTS DPR-IEWK-KIQDGGTTVVYFDNKI 84
Db 107 VNLKIYQKLTFKYAPTQETEGEDAVIICDVSSIPSIIITWRHKGD-----VIPKDV 161

Qy 85 QGDLAGTDFGKTSRLIMNVRTSDSAIYRCE--VVALNDRKEVDEITIELIVQKVP 142
Db 162 -----RFVVLANNYLQIRGIKKTKDEGNRCGRILA---RGEINYKDIQIVNVPELIQ 212

Qy 143 V--CRIPAAVPVGTATLQCOESGYPRPHYVYVRNDVPLPTDSRANPRFQNSGFVNSE 200
Db 213 ARQIRVNATANDSEVVLSC-DADGFPDPPEISLWKKEPIEDGE-----EKISF--NED 263

Qy 201 TGTLVFNAVHKDDSGQYCYIASNDAGAA 228
Db 264 KSEMTIYVRKEDAEAYSCIANNOAGEA 291
```

Search completed: June 15, 2004, 11:03:39
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 10:58:19 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRLRLRLYLPHFL.....VNYIRTSEGDPRHKSFFV 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTEMBL.25.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriapi.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1615	98.9	310	11 Q9BPK4	Q9BPK4 mus musculus
2	1604	98.2	310	11 Q9D8B7	Q9D8B7 mus musculus
3	1603	98.2	310	11 Q9D1M9	Q9D1M9 mus musculus
4	1409	86.3	310	4 Q9BX67	Q9BX67 homo sapien
5	1409	86.3	355	4 Q8WWL8	Q8WWL8 homo sapien
6	1400	85.7	309	4 Q96FL1	Q96FL1 homo sapien
7	497.5	30.5	298	11 Q9J159	Q9J159 mus musculus
8	494.5	30.3	298	11 Q8CE95	Q8CE95 mus musculus
9	494.5	30.3	298	11 Q8CE95	Q8CE95 mus musculus
10	450.5	27.6	300	11 Q9JHY1	Q9JHY1 rattus norv
11	447.5	27.4	300	11 Q8VC39	Q8VC39 mus musculus
12	426	25.1	289	13 Q7ZWT0	Q7ZWT0 xenopus lae
13	409.5	25.1	300	13 Q7SVQ7	Q7SVQ7 xenopus lae
14	340	20.8	259	4 Q9V5B2	Q9V5B2 homo sapien
15	336	20.6	64	11 Q8ST59	Q8ST59 mus musculus
16	321	19.7	173	11 Q9JKD5	Q9JKD5 rattus norv

17	257	15.7	318	13 Q91664	Q91664 xenopus lae
18	246.5	15.1	319	11 Q922D5	Q922D5 mus musculus
19	240.5	14.7	319	11 Q9JKA5	Q9JKA5 mus musculus
20	219	13.4	325	4 Q95791	Q95791 homo sapien
21	217.5	13.3	304	11 Q9CVA4	Q9CVA4 mus musculus
22	214	13.1	335	13 Q9PMR4	Q9PMR4 gallus gall
23	213	13.0	284	4 Q9NX42	Q9NX42 homo sapien
24	213	13.0	327	4 Q961Q7	Q961Q7 homo sapien
25	212	13.0	328	11 Q9Z1O9	Q9Z1O9 mus musculus
26	209.5	12.8	335	13 Q9YGH1	Q9YGH1 gallus gall
27	208	12.7	335	13 Q9YGV5	Q9YGV5 gallus gall
28	199	12.2	181	13 Q91665	Q91665 xenopus lae
29	197.5	12.1	387	4 Q86XK7	Q86XK7 homo sapien
30	197	12.1	259	4 Q7Z2Q1	Q7Z2Q1 homo sapien
31	193	11.8	372	13 Q90Y50	Q90Y50 brachydanio
32	192.5	11.7	407	11 Q9D2J4	Q9D2J4 mus musculus
33	190.5	11.7	248	11 Q9D0T4	Q9D0T4 mus musculus
34	185.5	11.4	795	13 Q90YM0	Q90YM0 brachydanio
35	185.5	11.4	1409	13 Q8J127	Q8J127 brachydanio
36	185.5	11.4	1409	13 Q801M2	Q801M2 brachydanio
37	185.5	11.4	1428	13 Q8AY67	Q8AY67 brachydanio
38	182.5	11.2	358	13 Q90490	Q90490 brachydanio
39	181	11.1	725	13 Q73633	Q73633 xenopus lae
40	180.5	11.1	838	13 Q90YM1	Q90YM1 brachydanio
41	179	11.0	181	11 Q9CWD9	Q9CWD9 mus musculus
42	178	10.9	416	4 Q8N7I3	Q8N7I3 homo sapien
43	177.5	10.9	298	13 Q804R4	Q804R4 brachydanio
44	177.5	10.9	1031	13 Q90YM2	Q90YM2 brachydanio
45	176.5	10.8	300	11 Q9DA22	Q9DA22 mus musculus

ALIGNMENTS

RESULT 1

Q9BPK4 PRELIMINARY; PRT; 310 AA.

AC Q9BPK4; (TREMREL. 16, Created)

DT 01-MAR-2001 (TREMREL. 16, Last sequence update)

DT 01-MAR-2001 (TREMREL. 16, Last sequence update)

DT 01-OCT-2003 (TREMREL. 25, Last annotation update)

DB Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)

DB Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)

DB Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)

GN JAM3 OR JAM2 OR JAM2 OR JAM-2 OR 1110002N23Rik.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=11036763;

RA Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;

RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular

RT Family?";

RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA	Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pasole G., Quackenbush J.,
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA	Blake J., Moffelli D., Bojunga N., Carninci P., de Bonaldi M.P.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUR=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AJ300304; CAC20704.1; -
DR EMBL; AK013156; BAB28683.1; -
DR EMBL; BC024357; AAH24357.1; -
DR EMBL; AK032833; BAC28049.1; -
DR MGD; MGI:1933825; Jam3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34937 MW; 4892BCB51D0A4B0A CRC64;

Query Match 98.9%; Score 1615; DB 11; Length 310;
Best Local Similarity 99.4%; Pred. No. 1.1e-152;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLPHFFLLLPFGCMIEAVNLKSSNRNPVVFHESVELSCIITHSQT 60
Db 1 MALSRRLRLRLYLPHFFLLLPFGCMIEAVNLKSSNRNPVVFHESVELSCIITDSQT 60

Qy 61 SDPIEWKIKDQGTYYVFNKIQGLDAGTDVFGKTSLRIMWVTRSDSAIYCEVVAL 120
Db 61 SDPIEWKIKDQGTYYVFNKIQGLDAGTDVFGKTSLRIMWVTRSDSAIYCEVVAL 120

Qy 121 NDRKEVDIITELIVQVKPVPVCRIPAAVPVGTATLQCOSESGYPRPHYSWYRNDVPL 180
Db 121 NDRKEVDIITELIVQVKPVPVCRIPAAVPVGTATLQCOSESGYPRPHYSWYRNDVPL 180

Qy 181 PTDGRANPRFQNSFFHNSSETGLVFNVAHKDSDGQYCIASNDAGAARCEGDMEVYDL 240
Db 181 PTDGRANPRFQNSFFHNSSETGLVFNVAHKDSDGQYCIASNDAGAARCEGDMEVYDL 240

Qy 241 NIAGIGGLVVLVLAVITMGICCAVRRGCFISSKQDGSYKSPGKHGDNVYRTISEG 300
Db 241 NIAGIGGLVVLVLAVITMGICCAVRRGCFISSKQDGSYKSPGKHGDNVYRTISEG 300

Qy 301 DFRHKSFEVI 310
Db 301 DFRHKSFEVI 310

RESULT 2
Q9DB87 PRELIMINARY; PRT; 310 AA.
AC Q9DB87;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUR=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kleitschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

Query Match 98.2%; Score 1604; DB 11; Length 310;
Best Local Similarity 98.7%; Pred. No. 1.4e-151;
Matches 306; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MALSRRLRLRLYLPHFFLLLPFGCMIEAVNLKSSNRNPVVFHESVELSCIITHSQT 60
Db 1 MALSRRLRLRLYLPHFFLLLPFGCMIEAVNLKSSNRNPVVFHESVELSCIITDSQT 60

Qy 61 SDPIEWKIKDQGTYYVFNKIQGLDAGTDVFGKTSLRIMWVTRSDSAIYCEVVAL 120
Db 61 SDPIEWKIKDQGTYYVFNKIQGLDAGTDVFGKTSLRIMWVTRSDSAIYCEVVAL 120

Qy 121 NDRKEVDIITELIVQVKPVPVCRIPAAVPVGTATLQCOSESGYPRPHYSWYRNDVPL 180
Db 121 NDRKEVDIITELIVQVKPVPVCRIPAAVPVGTATLQCOSESGYPRPHYSWYRNDVPL 180

Qy 181 PTDGRANPRFQNSFFHNSSETGLVFNVAHKDSDGQYCIASNDAGAARCEGDMEVYDL 240
Db 181 PTDGRANPRFQNSFFHNSSETGLVFNVAHKDSDGQYCIASNDAGAARCEGDMEVYDL 240

Qy 241 NIAGIGGLVVLVLAVITMGICCAVRRGCFISSKQDGSYKSPGKHGDNVYRTISEG 300
Db 241 NIAGIGGLVVLVLAVITMGICCAVRRGCFISSKQDGSYKSPGKHGDNVYRTISEG 300

Qy 301 DFRHKSFEVI 310
Db 301 DFRHKSFEVI 310

RESULT 3
Q9D1M9 PRELIMINARY; PRT; 310 AA.
AC Q9D1M9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.


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QY 241 NIAGTGGVLLVLLVAVITWGICCAVRRGCTISSKODGESYKSPGKHGDNVYRTSEEG 300
DB 241 NIGGIIGGVLLVLLVAVLALITLGICCAVRRGYFINNKODGESYKSPGKHGDNVYRTDEEG 300

QY 301 DFRKSSFVI 310
DB 301 DFRKSSFVI 310

RESULT 5
Q8WVL8 PRELIMINARY; PRT; 355 AA.
AC Q8WVL8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction adhesion molecule 3.
GN JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hearn T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Phillips H.M.;
RT "Narrowing the critical region within 11q24-qter for hypoplastic left
RT heart and identification of a candidate gene, JAM3, expressed during
RT cardiogenesis.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416101; CAC94776.1; -.
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Immunoglobulin domain.
PT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.
SQ SEQUENCE 355 AA; 39602 MW; 8B1577D8A7B1D4F8 CRC64;

Query Match 86.3%; Score 1409; DB 4; Length 355;
Best Local Similarity 85.8%; Pred. No. 5e-132;
Matches 266; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALSRLRLRLYLRLPHFFLLLLFRGCMIEAVNLKSSNRNPVVFESVLSCLIIHSTQ 60
DB 46 MALRRPRLRLCARLPDPFFLLLLFRGCLIGAVNLKSSNRTPVVOEFESVLSCLIIHSTQ 105

QY 61 SDPRIWKIKIQDQTTVVYFDNKGDLAGRTDVGKTSRLRWVTRSDSALYRCRVVAL 120
DB 106 SDPRIWKIKIQDQTTVVYFDNKGDLAGRAELIGKTSRLRWVTRSDSALYRCRVAR 165

QY 121 NDRKEVDSEITIELIVQVKPTVPCRIPAAPVPGKATLQCSSEGYRPHYSWYRNDVPL 180
DB 166 NDRKEIDSEIVELTVQVKPTVPCRVKAPVPGKMATLHCQSEGHPRPHYSWYRNDVPL 225

QY 181 PDSRANPRPNSSPHVNSTGTLVFNVAHKDQSGQYTCIASNDAGARCEQDMVEYDL 240
DB 226 PDSRANPRPNSSPHVNSTGTLVFNVAHKDQSGQYTCIASNDAGARCEQDMVEYDL 285

QY 241 NIAGTGGVLLVLLVAVITWGICCAVRRGCTISSKODGESYKSPGKHGDNVYRTSEEG 300
DB 286 NIGGIIGGVLLVLLVAVLALITLGICCAVRRGYFINNKODGESYKSPGKHGDNVYRTDEEG 345

QY 301 DFRKSSFVI 310
DB 346 DFRKSSFVI 355

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RESULT 6
Q96FL1 PRELIMINARY; PRT; 309 AA.
AC Q96FL1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010690; AAH10690.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
PT HYDROPHOBIC 1
SQ SEQUENCE 309 AA; 34917 MW; 50CSB1B7872E8DF3 CRC64;

Query Match 85.7%; Score 1400; DB 4; Length 309;
Best Local Similarity 85.4%; Pred. No. 3.3e-131;
Matches 264; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

QY 2 ALSRLRLRLYLRLPHFFLLLLFRGCMIEAVNLKSSNRNPVVFESVLSCLIIHSTQ 61
DB 1 ALRRPRLRLCARLPDPFFLLLLFRGCLIGAVNLKSSNRTPVVOEFESVLSCLIIHSTQ 60

QY 62 DPRIENKKIQDQTTVVYFDNKGDLAGRTDVGKTSRLRWVTRSDSALYRCRVVAL 121
DB 61 DPRIENKKIQDQTTVVYFDNKGDLAGRAELIGKTSRLRWVTRSDSALYRCRVARN 120

QY 122 DRKEVDSEITIELIVQVKPTVPCRIPAAPVPGKATLQCSSEGYRPHYSWYRNDVPL 181
DB 121 DRKEIDSEIVELTVQVKPTVPCRVKAPVPGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 182 TDSRANPRPNSSPHVNSTGTLVFNVAHKDQSGQYTCIASNDAGARCEQDMVEYDL 241
DB 181 TDSRANPRPNSSPHVNSTGTLVFNVAHKDQSGQYTCIASNDAGARCEQDMVEYDL 240

QY 242 IAGIIGGVLLVLLVAVITWGICCAVRRGCTISSKODGESYKSPGKHGDNVYRTSEEG 301
DB 241 IGGIIGGVLLVLLVAVLALITLGICCAVRRGYFINNKODGESYKSPGKHGDNVYRTDEEG 300

QY 302 FRKSSFVI 310
DB 301 FRKSSFVI 309

RESULT 7
Q9J159 PRELIMINARY; PRT; 298 AA.
AC Q9J159;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vascular endothelial junction-associated molecule (Junctional adhesion molecule-3) (2410030G21RIK protein).
GN JAM2 OR JAM3 OR JAM2 OR JAM-3 OR 2410030G21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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Db      288 NDFKHTKSP11 298

RESULT 8
Q8C895 PRELIMINARY; PRT; 298 AA.
ID Q8C895
AC Q8C895;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DB Junction cell adhesion molecule 2.
GN JAM2 OR JCAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002) .
DR EMBL; AK028757; BAC26102.1; -.
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00835; IGV_LIKE; 2.
SQ SEQUENCE 298 AA; 33079 MW; CB8227BC13D349A3 CRC64;

Query Match 30.3%; Score 494.5; DB 11; Length 298;
Best Local Similarity 37.0%; Pred. No. 8.4e-41;
Matches 115; Conservative 54; Mismatches 115; Indels 27; Gaps 9;

Qy 13 ARLPHPFLLLFRGMIRAVNLKSN-----RNVVHPFESVELSCIIITHSQTS DP 63
Db 2 ARSPQGLLMLLHLHYLIVADYHKANGFSASKDHRQEVTVIEPQAILAC-KTPKKTSS 60
Qy 64 RIWKKIQDQYTVYFDNKIQGLAGRTDVPKTSIRIWNVTRSDSAIYRCVEVALNDR 123
Db 61 RLEWKKVGQG-VSLVYVYQALQDGFDRABMI--DFNIRIKNVTRSDAGYRCVSAPT EQ 118
Qy 124 -KEVDTEITELIVQVXPVTPVCRIIPAAPVPGTKATLQCESEGYRPHYSWYRNDVPLPT 182
Db 119 GQNLQEDKQKWLKVLNAPNAPACEVPTSVMTGVSVEILRCQDKGNPAPEYIWFKDG----T 174
Qy 183 DSRANPR---FQNSPHVNSETGLVFNVAHKDDSGQYCYCIASNDAGAARCEQDMEVYD 239
Db 175 SLLGNPKGGTHNNSYTMNTKSGILQFNMIKMDSGEYTCARNVSGHRRCPCKRMQVDV 234
Qy 240 LNTAGLIGGVVLVYLIVLAVITWGIICCAIRGCGFISKQDGESYKSPKHGQGVNYITSEE 299
Db 235 LNTSGLIATVWVAFVISVCSGLGTCTYQARKGYF--SKTSTFQKQSP-----ASKVTWSE 287
Qy 300 GDFRHKSKSFVI 310
Db 288 NDFKHTKSP11 298

RESULT 9
Q8C5K9 PRELIMINARY; PRT; 298 AA.
ID Q8C5K9
AC Q8C5K9;
DT 01-MAR-2003 (TEMBLrel. 23, Created)

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KW Hypothetical protein.
SQ SEQUENCE 300 AA; 32423 MW; 3CB561B8FF3B97EC CRC64;

Query Match
Best Local Similarity 34.2%; Score 447.5; DB 11; Length 300;
Matches 102; Conservative 63; Mismatches 118; Indels 15; Gaps 7;

QY 20 LLLPRGCMIEAV-----NLKSNRPVNVHFESEVELSCIIITHSQTSDPRIEWKKIQDQ 74
DB 11 LFLFTSMILGSLVQKGSVYTAQSDVQPNESIKLTC--TSGFSSPRVWKFVQGST 68

QY 75 TTYVYFDNKIQDGLAGRTDVGKTSLRITWNTSDSAIYRCVWALNDRKVEITIELI 134
DB 69 TALVCYNSQITAPYADRV--TFSSGITFSSTVRKNGEYTC-WVSEEGQNTGEVSIHIT 126

QY 135 VQVKVTPVCRIPAAVPVCKTATLQCBSEGYPRPHYSWYRDVPLPT--DSRANPRFQNS 193
DB 127 VLVPPSKPTISVPSSVTIGRAVLTCSEHDGPPSEYSWFKDGIKMLTADAKKTRAPWNS 186

QY 194 SFVNSSETGLVFNVAHKDDSGYYCIASNDAGAA--RCGQDMEVYDLNAGIIGVLV 252
DB 187 SFTIDPKGDLIFDPVTAFDSEGYCQAQNGYGTAMRSEAHMDAVELNVGIGVAAVLVT 246

QY 253 LIVLAVITNGICAYRGCFFISKQDGSYKSPGKHGYNVYIRTSEGDPRHKSSPVI 310
DB 247 LILLGLLIFGVWFAYSRGYFERTKGG---TAPGRKVIYSQPSRSEGEFKQTSFLV 300

RESULT 12
Q7ZWTO PRELIMINARY; PRT; 289 AA.
AC Q7ZWTO
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Similar to junctional adhesion molecule 1.
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046720; AAH46720.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 289 AA; 31630 MW; 2435485A37618845 CRC64;

Query Match
Best Local Similarity 34.0%; Score 426; DB 13; Length 289;
Matches 98; Conservative 57; Mismatches 113; Indels 20; Gaps 8;

QY 27 CMIEAVNLKS--SNRNP--VHFESEVELSCIIITHSQTSDPRIEWKKI--QDQTTYVYFN 82
DB 18 CCLWTVTLAAVTTPNTIIVKESAEALQCSYSSDFTS--PRVEMKFNVDQETSFFVYD 76

QY 83 KIQGLAGRTDVGKTSLRITWNTSDSAIYRCVWALNDRKVEITIELIVQKVPVTP 142
DB 77 SITAPVKDRAIPFPQ--GITLKQITRKDAGEYSCEVTSTGSKLYGKAIQLQVIVAPSP 135

QY 143 VCRIPAAVPVCKTATLQCBSEGYPRPHYSWYRDVPLPTDSRANPRFQNSFFVNSETG 202
DB 136 VAQVPRSVSTGSAVALLCVENDGYPPTFTIYENKSPM---QIAP--QNSTTIDPKTG 189

QY 203 TLVFNVAHKDDSGYYCIASNDAGAACRCGQDMEVYDLNAGIIGVLVILVAVITMG 262

Db 190 VLKFAAVSTSDSGEYICRATNNGQKQASDLVRMDVQDVNVGGVAAVIVLLIALIGFG 249
QY 263 ICCAYRGCFFISKQDGSYKSPGKHGYNVYIRTSEGDPRHKSSPVI 310
DB 250 MWFAYSRGVLDKRNKKKVIYSLPSE-----TRSDKNFQQTSSFLV 289

RESULT 13
Q7SYQ7 PRELIMINARY; PRT; 300 AA.
AC Q7SYQ7
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.F., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054305; AAH54305.1;
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 300 AA; 32858 MW; 02BC49DC74E271D4 CRC64;

Query Match
Best Local Similarity 33.1%; Score 409.5; DB 13; Length 300;
Matches 90; Conservative 55; Mismatches 104; Indels 23; Gaps 6;

QY 43 VHEFSEVELSCIIITHSQTSD---PRIEWKKI--QDQTTYVYFNKIQDGLAGRTDVGPKT 98
DB 48 VKEGSDPLRC---SYTSDYINPRVEMKFNVDQETSFFVYDGLSTASYKDRATSPQ- 102

QY 99 SLRIWNTSDSAIYRCVWALNDRKVEITIELIVQKVPVTPVCRIPAAVPVGTATL 158
```

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Db 103 GIKLQVTRKDAGEYSCEVTSCTGVLYGEAKIQLVIVAPGTPVAQVPSSARTGSVAEL 162
Qy 159 QCQSESGYPRPHYSWYNDVPLPTDSRANPRFONSSPHVNSECTGLVFNVAHVHDDSGQYY 218
Db 163 MCVEIQGFPLPTFWYHNSFMQAKS-----QNSTYTDPTNGVLKFAVSGTSDSGEYY 216
Qy 219 CIASNDAGARCEQDMEVVDLNIAGHIGGVLLVILVAVITMGICCAVRRGCFISSKQD 278
Db 217 CKATNSQEQSSAIVRMDVXVNVGGIVAAVIVLLILALLGLFGLMPAYSRGVILDRKGNK 276
Qy 279 GESYKSPGKHGDNVYIRTSSEGDPRHKS SFVI 310
Db 277 KVIYSQPSB-----TRSDKNFQOTSSFLV 300
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RESULT 14

```
QY5B2 PRELIMINARY; PRT; 259 AA.
AC QY5B2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction adhesion molecule.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Nusrat A., Schnell F.J., Walsh S., Reeves T.A., Pochet M.,
RA Foley C., Parks C.A.;
RT "Human junctional adhesion molecule is expressed by polarized columnar
RT epithelia and regulates tight junction resealing."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF154005; AAD43794.1;
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_C2.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PS0835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 259 AA; 28122 MW; FE38521A911582D0 CRC64;
```

```
Query Match 20.8%; Score 340; DB 4; Length 259;
Best Local Similarity 30.9%; Pred. No. 1.9e-25;
Matches 84; Conservative 48; Mismatches 106; Indels 34; Gaps 7;

Qy 42 VVHEFESVLSLIITHSOTSDPRIEWKKIQDQTYVYFONKIQGLAGRTDVPFGKTSLR 101
Db 19 ILPENNVPKUSC--AYSGFSFRA-----ASYEDRV-----TFLPTGIT 55

Qy 102 IWNVTRSDSAIYRCVVALANDRKEVDITBLIVQVAPVTPVCRIPAAVPVGTATLQCC 161
Db 56 FKSVTREDTGTYTC-MVPEEGNSYGEVKVLLVLVPPSKPTVNIIPSSATIGNRAVLTC 114

Qy 162 ESEGYPRPHYSWYNDVPLPTDSRANPRFONSSPHVNSECTGLVFNVAHVHDDSGQYYCIA 221
Db 115 EQDGSPPSEYTWFKDGIWMTNPKSTAFNSSYVLNPTTGELVFDPLSLASDTGEYSCEA 174

Qy 222 SNDAGARCEQ-DMEVVDLNIAGHIGGVLLVILVAVITMGICCAVRRGCFISSKQDGB 280
Db 175 RNYGTPTMTNANVMEAVERNVGVVAVLVLTLLGLLVFGIWPAYSRGHFDRKKGTS 234

Qy 281 SYKSPGKHGDNVYIRTS--REGDPRHKS SFVI 310
Db 235 SKK-----VYISQPSARSEGEFKQTS SFV 259
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RESULT 15

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Q8BT59 PRELIMINARY; PRT; 64 AA.
ID Q8BT59
AC Q8BT59;
```

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DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Junction cell adhesion molecule 3 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK017692; BAC25526.1; -.
FT NON TER 1
SQ SEQUENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;

Query Match 20.6%; Score 336; DB 11; Length 64;
Best Local Similarity 100.0%; Pred. No. 7.1e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 GGVLVVLVILVAVITMGICCAVRRGCFISSKQDGSYKSPGKHGDNVYIRTSSEGDPRHKS 306
Db 1 GGVLVVLVILVAVITMGICCAVRRGCFISSKQDGSYKSPGKHGDNVYIRTSSEGDPRHKS 60

Qy 307 SFVI 310
Db 61 SFVI 64

Search completed: June 15, 2004, 11:05:05
Job time : 38 secs
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PD 22-JUN-2000.
XX 01-DEC-1999; 99WO-US028634.
XX 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 98US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 98US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
XX (GETH) GENENTECH INC.
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WT;
XX MPI; 2000-431586/37.
DR N-PSDB; AAA51265.
XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT transmembrane polypeptide.
XX Claim 1; Fig 14; 154pp; English.
XX This is PRO1868, a putative homologue of A33 antigen, a known colorectal
CC cancer-associated marker. The invention concerns novel secreted and
CC transmembrane proteins, designated PRO polypeptides. The cDNA and gene
CC sequences are useful in the recombinant production of PRO polypeptides,
CC as a hybridization probe to screen libraries to isolate cDNAs with
CC sequence identity to PRO polypeptides or to map the gene encoding the PRO
CC polypeptides and analyzing genetic disorders. The cDNA/gene can also be
CC used to produce transgenic animals useful for the development and
CC screening of therapeutically useful reagents. They can also be used in
CC gene therapy, e.g. to replace a defective gene
XX Sequence 310 AA;
Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQPFPSVLSCLITDSQT 60
Db 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQPFPSVLSCLITDSQT 60
QY 61 SDPRLEWKIODEQTYTTFDNNKIOGDLGRAEILGKTSKIWNVTRDSALYRCEVVAR 120
Db 61 SDPRLEWKIODEQTYTTFDNNKIOGDLGRAEILGKTSKIWNVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVLTQVQKVPVTPVCRVPAVPVGRKATLHCQSEGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVLTQVQKVPVTPVCRVPAVPVGRKATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSANPRFRNSSPHLNSGTGLVFTAVHKDDSGQYTCIASNDAGSARCEQEYVDL 240
Db 181 PTDSANPRFRNSSPHLNSGTGLVFTAVHKDDSGQYTCIASNDAGSARCEQEYVDL 240
QY 241 NIGGIIGVLLVLAVALITLIGICAYRGGYFINKQDGSYKPKGPDGVNVIKTDREG 300
Db 241 NIGGIIGVLLVLAVALITLIGICAYRGGYFINKQDGSYKPKGPDGVNVIKTDREG 300
QY 301 DFRHKSSFFVI 310
Db 301 DFRHKSSFFVI 310

ID AAB33457 standard; protein; 310 AA.
XX AAB33457;
AC 29-JAN-2001 (first entry)
DT Human PRO1868 protein UNQ859 SEQ ID NO:193.
DE Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antiarthritis; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX Homo sapiens.
OS WO200053758-A2.
XX 14-SEP-2000.
PD 02-MAR-2000; 200WO-US005841.
PF 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 20-APR-1999; 99WO-US0128849P.
PR 28-APR-1999; 99WO-US008615.
PR 04-MAY-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0132371P.
PR 02-JUN-1999; 99US-0134287P.
PR 23-JUN-1999; 99WO-US012252.
PR 26-JUL-1999; 99US-0141037P.
PR 28-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020111.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 05-OCT-1999; 99WO-US021547.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028585.
PR 20-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 99WO-US031274.
PR 06-JAN-2000; 200WO-US000219.
PR 06-JAN-2000; 200WO-US000277.
PR 11-FEB-2000; 200WO-US003565.
PR 18-FEB-2000; 200WO-US004341.
PR 18-FEB-2000; 200WO-US004342.
PR 22-FEB-2000; 200WO-US004414.
XX (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX WPI: 2000-572271/53.
XX N-PSDB; AAC58622.
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX Claim 33; Fig 88; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention

XX SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSLCIITDSQT 60
DB 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSLCIITDSQT 60
QY 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMWVTRDSALYRCEVVAR 120
DB 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMWVTRDSALYRCEVVAR 120
QY 121 NDRKEIDRIVIELTVQVKPTVPCRVKAVPGKMATLHCQESGHPHYSWYRNDVPL 180
DB 121 NDRKEIDRIVIELTVQVKPTVPCRVKAVPGKMATLHCQESGHPHYSWYRNDVPL 180
QY 181 PTDGRANPRFNSFHLNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEYVDL 240
DB 181 PTDGRANPRFNSFHLNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEYVDL 240
QY 241 NIGGIIGVLVLAVALITLIGICAVYRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
DB 241 NIGGIIGVLVLAVALITLIGICAVYRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310

RESULT 3
AAB27276

ID AAB27276 standard; protein; 310 AA.

XX AC AAB27276;

XX DT 23-FEB-2001 (first entry)

XX DE Human confluency regulated adhesion molecule 1 #2.

XX KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
XX inflammation; cancer; wound; angiogenesis; human;
XX confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX OS Homo sapiens.
XX WPI: 2000-587436/55.
XX N-PSDB; AAA95306.
XX Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
XX CRAM-2) polypeptide, useful for treatment of tumors, inflammation
XX reactions and modulating vascular permeability.
XX Claim 2; Fig 6; 59pp; English.
XX The present sequence is the human confluency regulated adhesion molecule
XX 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
XX proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
XX and coding sequence can be used in the treatment of cancer, inflammation,
XX to modulate cell-cell interactions and angiogenesis, and in the
XX modulation of wound healing

SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSLCIITDSQT 60
DB 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSLCIITDSQT 60
QY 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMWVTRDSALYRCEVVAR 120
DB 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKIMWVTRDSALYRCEVVAR 120
QY 121 NDRKEIDRIVIELTVQVKPTVPCRVKAVPGKMATLHCQESGHPHYSWYRNDVPL 180
DB 121 NDRKEIDRIVIELTVQVKPTVPCRVKAVPGKMATLHCQESGHPHYSWYRNDVPL 180
QY 181 PTDGRANPRFNSFHLNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEYVDL 240
DB 181 PTDGRANPRFNSFHLNSETGLVFTAVHKDDSGQYVCIASNDAGSARCEQEYVDL 240
QY 241 NIGGIIGVLVLAVALITLIGICAVYRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
DB 241 NIGGIIGVLVLAVALITLIGICAVYRGYFINNKQDGSYKPKGPDGVNVRTDEEG 300
QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310

RESULT 4
AAB80272

ID AAB80272 standard; protein; 310 AA.

XX AC AAB80272;

XX DT 24-APR-2001 (first entry)

XX DE Human PRO1868 protein.
XX DE
XX KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
XX KW antiparkinsonian neurotropic; neuroprotective; vulnerary; cardian;
XX KW antiangiogenic; vasotropic; antiaesthatic; antiarthritis; cancer;
XX KW antiarthritis; antiinfertility; antidiabetic; antiviral; diabetes;
XX KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
XX KW ischaemia; inflammation.
XX OS Homo sapiens.
XX PN WO200104311-A1.
XX PD 18-JAN-2001.
XX PP 22-FEB-2000; 2000WO-US004414.
XX PR 07-JUL-1999; 99US-0143048P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 05-OCT-1999; 99WO-US023089.
XX PR 29-NOV-1999; 99WO-US028214.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Botstein D, Desnoyers L, Baton DL, Ferrara N;
XX PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen WB, Goddard A;
XX PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
XX PI Mather JP, Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D;
XX PI Williams PM, Wood WI;
XX DR WPI; 2001-081051/09.
XX DR N-PSDB; AAF72433.
XX PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
XX PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
XX PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
XX PT disease).
XX PS Claim 1; Fig 124; 393pp; English.
XX CC The present sequence is one of sixty one novel secreted and transmembrane
XX CC PRO polypeptides. The PRO polypeptides are useful for treating skin
XX CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
XX CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
XX CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
XX CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
XX CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
XX CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
XX CC infertility, AIDS and diabetes and retinal disorders such as retinitis
XX CC pigmentosa. The PRO nucleic acids have applications in molecular
XX CC biology, including use as hybridization probes, and in chromosome and
XX CC gene mapping
XX CC Sequence 310 AA;
XX CC
XX CC Query Match 100.0%; Score 310; DB 4; Length 310;
XX CC Best Local Similarity 100.0%; Pred. No. 1.6e-295;
XX CC Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC 1 MALRRPPLRLCARLPDFLLLLFRGCLTGAVNLKSSNRTPVVQEFSEVLSCTITDSQT 60
XX DB 1 MALRRPPLRLCARLPDFLLLLFRGCLTGAVNLKSSNRTPVVQEFSEVLSCTITDSQT 60
XX QY 61 SDPRLWKIKIDQRTTYVFFDNKIQGDLGRABEIIIGKTSKIWNTRDSALYRCVWAR 120
XX DB 61 SDPRLWKIKIDQRTTYVFFDNKIQGDLGRABEIIIGKTSKIWNTRDSALYRCVWAR 120
XX QY 121 NDRKEIDRIVIELTVQVKPVPVCRVPAVPGVMATLHCQSEBEGHPRPHYSWYRNDVPL 180
XX DB 121 NDRKEIDRIVIELTVQVKPVPVCRVPAVPGVMATLHCQSEBEGHPRPHYSWYRNDVPL 180
XX QY 181 PTDSRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
XX DB 181 PTDSRANPRFRNSSPHLNSSETGLVPTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
XX QY 241 NIGGIIGGVVLAVLALITIGICCAVRRGYPINNKKQDGSYKPKGPNVYIRTDSEG 300
XX DB 241 NIGGIIGGVVLAVLALITIGICCAVRRGYPINNKKQDGSYKPKGPNVYIRTDSEG 300
XX QY 301 DFRHKSSFVI 310
XX DB 301 DFRHKSSFVI 310
XX RESULT 5
XX ID AAM93905
XX AC AAM93905 standard; protein; 310 AA.
XX AC AAM93905;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide, SEQ ID NO: 4051.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX OS Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
XX N-PSDB; AAK94867.
XX 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
XX The invention relates to primers for synthesising full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesising the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a polypeptide encoded by a full length
XX human cDNA of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in CD-ROM
XX format directly from EPO

```
XX SQ Sequence 310 AA;
Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFSEVLSCLITDSQT 60
DB 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFSEVLSCLITDSQT 60
QY 61 SDPRIEMKKIQDSQTTVVFFDNKIQDLAGRAEILGKTSUKIWNVTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDSQTTVVFFDNKIQDLAGRAEILGKTSUKIWNVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEVYDL 240
QY 241 NIGGIIGGLVLAVALITLIGICCAVRGYPFNNKODGESYKPKPGDGVNVRTDEEG 300
DB 241 NIGGIIGGLVLAVALITLIGICCAVRGYPFNNKODGESYKPKPGDGVNVRTDEEG 300
QY 301 DFRHKSFSVI 310
DB 301 DFRHKSFSVI 310
RESULT 6
AAM93323
ID AAM93323 standard; protein; 310 AA.
XX AC AAM93323;
DT 06-NOV-2001 (first entry)
XX DE Human polypeptide, SEQ ID NO: 2845.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX OS Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-0018774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX DR N-PSDB; AAK94243.
XX DR WPI; 2001-524255/58.
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX PS Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
XX CC The invention relates to primers for synthesizing full length cDNA
XX CC clones. 830 cDNA molecules encoding a human protein have been isolated
XX CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX CC been determined. Primers for synthesizing the full length cDNA are useful
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CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX SQ Sequence 310 AA;
Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFSEVLSCLITDSQT 60
DB 1 MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFSEVLSCLITDSQT 60
QY 61 SDPRIEMKKIQDSQTTVVFFDNKIQDLAGRAEILGKTSUKIWNVTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDSQTTVVFFDNKIQDLAGRAEILGKTSUKIWNVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHPRHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFRNSSPHLNSGTGLVFTAVHKDSDGQYYCIASNDAGSARCEQEMEVYDL 240
QY 241 NIGGIIGGLVLAVALITLIGICCAVRGYPFNNKODGESYKPKPGDGVNVRTDEEG 300
DB 241 NIGGIIGGLVLAVALITLIGICCAVRGYPFNNKODGESYKPKPGDGVNVRTDEEG 300
QY 301 DFRHKSFSVI 310
DB 301 DFRHKSFSVI 310
RESULT 7
AAU12440
ID AAU12440 standard; protein; 310 AA.
XX AC AAU12440;
XX DT 24-OCT-2001 (first entry)
XX DE Human PRO1868 polypeptide sequence.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX KW A-peptide; factor VIIA; gene therapy.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.
XX PP 01-DEC-2000; 2000WO-US032678.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 30-DEC-1999; 99WO-US031243.
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PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US000365.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000WO-US017202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000WO-US0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21512.
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX Claim 12; Fig 538; 813pp; English.
PS AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX Sequence 310 AA;
SQ Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIITDSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIITDSQT 60
QY 61 SDPRIWKKIODEQTYYVFPDNKIQGDLAGRAEILGKTSLKINWVTRDSALYRCVVAR 120
DB 61 SDPRIWKKIODEQTYYVFPDNKIQGDLAGRAEILGKTSLKINWVTRDSALYRCVVAR 120
QY 121 NDRKEIDISIVIELTVQVKPVTFCRVKPAVPGKMATLHCQESGHPHRYGWNVDVPL 180
DB 121 NDRKEIDISIVIELTVQVKPVTFCRVKPAVPGKMATLHCQESGHPHRYGWNVDVPL 180
QY 181 PTDSRANPRFRNSPFLNSETGLVPTAVHKDDSGQYYCIAENNDAGSARCEQMEVVDL 240
DB 181 PTDSRANPRFRNSPFLNSETGLVPTAVHKDDSGQYYCIAENNDAGSARCEQMEVVDL 240
QY 241 NIGGIIGGVLVVLAVALITIGICCAVYRGYFINNKQDGSYKPKGPDGVNYYIRTDSEG 300
DB 241 NIGGIIGGVLVVLAVALITIGICCAVYRGYFINNKQDGSYKPKGPDGVNYYIRTDSEG 300
QY 301 DFRHKSSPVI 310
DB 301 DFRHKSSPVI 310
RESULT 8
AAB80383
ID AAB80383 standard; protein; 310 AA.
AC AAB80383;
XX 24-APR-2001 (first entry)
DT Secreted protein encoded by gene #13.
DE Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX Homo sapiens.
XX WO200107459-A1.
XX 01-FEB-2001.
XX 20-JUL-2000; 2000WO-US019735.
XX 23-JUL-1999; 99US-0145220P.
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX WPI; 2001-1233261/13.
DR New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX Claim 11; Page 538-539; 601pp; English.
XX The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angioneurosis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX Sequence 310 AA;
SQ

Query Match	100.0%; Score 310; DB 4; Length 310;
Best Local Similarity	100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQPSVLSCLITDSQT 60
Db	1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQPSVLSCLITDSQT 60
Qy	61 SDPRIWKKIODETQTVVFFDNKIQGDLAGRAELIGKTSLKIMNVTTRDSALYRCEVVAR 120
Db	61 SDPRIWKKIODETQTVVFFDNKIQGDLAGRAELIGKTSLKIMNVTTRDSALYRCEVVAR 120
Qy	121 NDRKEIDBIVELTVQVKPVPVCRKPAVPGKMATLHCQESGHPHYSWYRNDVPL 180
Db	121 NDRKEIDBIVELTVQVKPVPVCRKPAVPGKMATLHCQESGHPHYSWYRNDVPL 180
Qy	181 PTDSRANPRFNSSPHLNSGTGLVFAVHKDDSGQYYCTASNDAGSARCEEQEMEYVDL 240
Db	181 PTDSRANPRFNSSPHLNSGTGLVFAVHKDDSGQYYCTASNDAGSARCEEQEMEYVDL 240
Qy	241 NIGGIIGVLVLAVALILITGICCAYYRGYFINNKDGSYKNPKGPDGVNVRTDEEG 300
Db	241 NIGGIIGVLVLAVALILITGICCAYYRGYFINNKDGSYKNPKGPDGVNVRTDEEG 300
Qy	301 DFRHKSFEVI 310
Db	301 DFRHKSFEVI 310
RESULT 9	
AA880408	standard; protein; 310 AA.
XX	
AC	AA880408;
XX	
AC	
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Secreted protein encoded by gene #38.
XX	
DE	Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW	cardiovascular; infection; food.
KX	
XX	
OS	Homo sapiens.
XX	
PN	WO200107459-A1.
XX	
PD	01-FEB-2001.
XX	
PF	20-JUL-2000; 2000WO-US019735.
XX	
PR	23-JUL-1999; 99US-0145220P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI	Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX	
DR	WPI; 2001-123261/13.
XX	
PT	New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT	preventing and treating e.g. autoimmune, hyperproliferative,
PT	cardiovascular, and ocular diseases or disorders and microorganism
PT	infections.
XX	
PS	Claim 11; Page 557-558; 601pp; English.
XX	
CC	The present invention relates to 29 human secreted proteins. The
CC	invention is used to prevent autoimmune diseases e.g. rheumatoid
CC	arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC	liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC	disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC	e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC	fungi and ocular disorders e.g. corneal infection. Also used in food

CC	preparations
XX	
SQ	Sequence 310 AA;
	Query Match 100.0%; Score 310; DB 4; Length 310;
	Best Local Similarity 100.0%; Pred. No. 1.6e-295;
	Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MALRRPRLRLCARLPDPFLLLRGLICAVNLKSSNRTFPVQEPESVELSCIITDSQT 60
Dd	1 MALRRPRLRLCARLPDPFLLLRGLICAVNLKSSNRTFPVQEPESVELSCIITDSQT 60
Qy	61 SDPRIWKKIQQDROTTVPFDNKIQGDLAGRABILGKTSLKINVTTRDSALYRCVVAR 120
Dd	61 SDPRIWKKIQQDROTTVPFDNKIQGDLAGRABILGKTSLKINVTTRDSALYRCVVAR 120
Qy	121 NDRKEIDRIVELTVQVKPTVCRVPKAPVCMMATLHCQSESGHPRPHYSWYRNVDVL 180
Dd	121 NDRKEIDRIVELTVQVKPTVCRVPKAPVCMMATLHCQSESGHPRPHYSWYRNVDVL 180
Qy	181 PTDSRANPRFRNSSFHLNSTGLTFTAVHKDDSGQYYCIASNDAGSARCEEQEVEYIDL 240
Dd	181 PTDSRANPRFRNSSFHLNSTGLTFTAVHKDDSGQYYCIASNDAGSARCEEQEVEYIDL 240
Qy	241 NIGGIIGGVLVLAVALITLGICCAIRRGYPINNKGDESYNPKPGDGNNYVRTDEEG 300
Dd	241 NIGGIIGGVLVLAVALITLGICCAIRRGYPINNKGDESYNPKPGDGNNYVRTDEEG 300
Qy	301 DFRHKSSFVI 310
Dd	301 DFRHKSSFVI 310
RESULT 10	
AAB80409	
ID	AAB80409 standard; protein; 310 AA.
XX	AAB80409;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Secreted protein encoded by gene #39.
KW	Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW	cerebrovascular; infection; food.
XX	
OS	Homo sapiens.
XX	
PN	WO200107459-A1.
XX	
PD	01-FEB-2001.
XX	
PF	20-JUL-2000; 2000WO-US019735.
XX	
PR	23-JUL-1999; 99US-0145220P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
Pf	Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
Pf	Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX	
DR	WPI; 2001-123261/13.
XX	
PT	New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT	preventing and treating e.g. autoimmune, hyperproliferative,
PT	cardiovascular, and ocular diseases or disorders and microorganism
XX	infections.
PS	
PS	Claim 11; Page 559-560; 601pp; English.
CC	The present invention relates to 29 human secreted proteins. The
CC	invention is used to prevent autoimmune diseases e.g. rheumatoid
CC	arthritis, hyperproliferative disorders e.g. neoplasms of the breast or

CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. Also used in food
 CC preparations
 XX
 SQ Sequence 310 AA;
 Query Match 100.0%; Score 310; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.6e-295;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQSFESVELSCIITDSQT 60
 DB 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQSFESVELSCIITDSQT 60
 QY 61 SDPRIEMKKIQDEQTTVYVFDNKKIQDLAGRAEILGKTSLKINWTRDSALYRCEVVAR 120
 DB 61 SDPRIEMKKIQDEQTTVYVFDNKKIQDLAGRAEILGKTSLKINWTRDSALYRCEVVAR 120
 QY 121 NDRKEIDIVIELTVQVKPVPVPCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
 DB 121 NDRKEIDIVIELTVQVKPVPVPCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSCQYTCIASNDAGSARCEQEHEVYDL 240
 DB 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSCQYTCIASNDAGSARCEQEHEVYDL 240
 QY 241 NIGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKPKDGVNVIITDREG 300
 DB 241 NIGGIIGVVLVLAVALITLIGICAYRRGYFINNKQDGESYKPKDGVNVIITDREG 300
 QY 301 DFRKXSSFYI 310
 DB 301 DFRKXSSFYI 310
 RESULT 11
 ABG92709
 ID ABG92709 standard; protein; 310 AA.
 AC ABG92709;
 DT 18-NOV-2002 (first entry)
 XX Human secreted protein PRO1868.
 KW Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
 KW PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
 KW inflammatory disorder; immune related disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
 KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
 KW psoriasis; allergic disease of the lung; graft-versus host disease;
 KW tumour; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN US2002098506-A1.
 XX
 PD 25-JUL-2002.
 XX
 PF 27-DEC-2001; 2001US-00033301.
 XX
 PR 04-AUG-1998; 98US-0095325P;
 PR 16-DEC-1998; 98US-0112851P;
 PR 16-DEC-1998; 98US-0113145P;
 PR 22-DEC-1998; 98US-0113511P;
 PR 12-JAN-1999; 99US-0115558P;
 PR 12-JAN-1999; 99US-0115565P;
 PR 09-FEB-1999; 99US-0115733P;
 PR 10-FEB-1999; 99US-0119341P;
 PR 12-FEB-1999; 99US-0119537P;
 PR 12-FEB-1999; 99US-0119965P;

PR 02-JUN-1999; 99WO-US012252.
 PR 29-OCT-1999; 99US-0162506P.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-FEB-2000; 2000WO-US003555.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000US-0187202P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 25-MAY-2001; 2001US-00866034.
 XX (GETH) GENENTECH INC.
 XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WI;
 XX WPI; 2002-690475/74.
 DR N-PSDB; ABS68392.
 XX Novel secreted and transmembrane polypeptides and polynucleotides useful
 PT for diagnosis and treatment of inflammatory disorders and immune-related
 PT diseases, and identifying modulators.
 XX Claim 12; Fig 14; 135pp; English.
 PS The invention relates to an isolated polypeptide having at least 80%
 CC amino acid sequence identity to secreted and transmembrane polypeptides
 CC PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
 CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
 CC cells and antibodies against PRO polypeptides. PRO proteins are useful
 CC for identifying modulators of the polypeptide. PRO1868 useful for the
 CC diagnosis and treatment of inflammatory and immune related diseases
 CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
 CC sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
 CC infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
 CC versus host disease and tumours. PRO nucleic acids are useful for
 CC constructing hybridisation probes for mapping the gene that encodes that
 CC PRO and for the genetic analysis of individuals with genetic disorders.
 CC and for generating transgenic animals which are useful in the development
 CC and screening of therapeutically useful reagents. PRO nucleic acids are
 CC also useful for gene therapy, chromosome identification, and tissue
 CC typing. PRO proteins are useful as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies are useful in
 CC diagnostic assays for PRO, e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO. The present
 CC sequence represents a PRO protein
 XX
 SQ Sequence 310 AA;
 Query Match 100.0%; Score 310; DB 5; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.6e-295;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQSFESVELSCIITDSQT 60
 DB 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVVQSFESVELSCIITDSQT 60
 QY 61 SDPRIEMKKIQDEQTTVYVFDNKKIQDLAGRAEILGKTSLKINWTRDSALYRCEVVAR 120
 DB 61 SDPRIEMKKIQDEQTTVYVFDNKKIQDLAGRAEILGKTSLKINWTRDSALYRCEVVAR 120
 QY 121 NDRKEIDIVIELTVQVKPVPVPCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
 DB 121 NDRKEIDIVIELTVQVKPVPVPCVRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
 QY 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSCQYTCIASNDAGSARCEQEHEVYDL 240
 DB 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDDSCQYTCIASNDAGSARCEQEHEVYDL 240

QY 241 NIGGIIGGVLVAVLALITLIGICCAVRGYFINNKQDGSYKXNPKGPDGVNVRTDEBG 300
 DB 241 NIGGIIGGVLVAVLALITLIGICCAVRGYFINNKQDGSYKXNPKGPDGVNVRTDEBG 300

QY 301 DFRHKSFSVI 310
 DB 301 DFRHKSFSVI 310

RESULT 12

ID ABG91361 standard; protein; 310 AA.

XX AC ABG91361;

DT 29-NOV-2002 (first entry)

XX DE Novel human secreted protein #7.

XX Human; secreted protein; transmembrane protein; gene mapping; transgenic; immunogenic.

XX OS Homo sapiens.

XX PN US2002098505-A1.

XX PD 25-JUL-2002.

XX PF 28-DEC-2001; 2001US-00033246.

XX PR 04-AUG-1998; 98US-0095325P.

XX PR 16-DEC-1998; 98US-0112851P.

XX PR 16-DEC-1998; 98US-0113145P.

XX PR 22-DEC-1998; 98US-0113511P.

XX PR 12-JAN-1999; 99US-0115558P.

XX PR 12-JAN-1999; 99US-0115565P.

XX PR 09-FEB-1999; 99US-0119341P.

XX PR 10-FEB-1999; 99US-0119537P.

XX PR 12-FEB-1999; 99US-0119665P.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 01-DEC-1999; 99WO-US028634.

XX PR 02-DEC-1999; 99WO-US028551.

XX PR 09-DEC-1999; 99US-0170262P.

XX PR 11-FEB-2000; 2000WO-US003565.

XX PR 22-FEB-2000; 2000WO-US004414.

XX PR 02-MAR-2000; 2000WO-US005841.

XX PR 30-MAR-2000; 2000US-0187202P.

XX PR 30-MAR-2000; 2000WO-US008439.

XX PR 02-JUN-2000; 2000WO-US014941.

XX PR 01-DEC-2000; 2000WO-US015264.

XX PR 25-MAY-2001; 2001US-00866034.

XX (GETH) GENENTECH INC.

XX Botstein D, Deanoysers L, Ferrara N, Fong S, Gao W, Goddard A;

XX Gurney AU, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;

XX Wood WI;

XX WPI; 2002-665999/71.

XX N-PSDB; ABS67460.

XX New human secreted and transmembrane (PRO) polypeptides, useful for

XX treating conditions requiring PRO polypeptides, for screening PRO

XX antagonists and agonists useful as drug candidates.

XX Claim 12; Fig 14; 125pp; English.

XX The invention relates to new human secreted and transmembrane proteins

XX (PRO) and nucleic acids of the invention. The polypeptides can be

CC

CC administered therapeutically, especially by expressing encoding
 CC polynucleotides, e.g. in therapeutic compositions. They can be used to
 CC screen for PRO polypeptide antagonists and agonists useful to identify
 CC drug candidates. They can also be used to produce antibodies, useful to
 CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
 CC therapeutically (e.g. as antagonists or to target and/or deliver
 CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
 CC produce antisense sequences to inhibit polypeptide production. They can
 CC be used to produce probes and primers useful to detect or isolate
 CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
 CC sequences from other species. They are also useful for gene mapping and
 CC to generate transgenic animals. ABG91355-ABG91363 represent human PRO
 CC amino acid sequences of the invention
 XX
 SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 5; Length 310;

Best Local Similarity 100.0%; Pred. No. 1.6e-295; Indels 0; Gaps 0;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 SDPRIWKKIODEQTYYVFDNKIQGLAGRAELGKTSKIMNVTTRDSALYRCEVVAR 120

DB 61 SDPRIWKKIODEQTYYVFDNKIQGLAGRAELGKTSKIMNVTTRDSALYRCEVVAR 120

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DB 181 PTDSRANPRFNSSPHLNSGTGLVFTAVHKDQSGYYCTASNDAGSARCEQEMVYDL 240

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DB 241 NIGGIIGGVLVAVLALITLIGICCAVRGYFINNKQDGSYKXNPKGPDGVNVRTDEBG 300

QY 301 DFRHKSFSVI 310

DB 301 DFRHKSFSVI 310

RESULT 13

ABB84947

ID ABB84947 standard; protein; 310 AA.

XX AC ABB84947;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO1868 protein sequence SEQ ID NO:262.

XX Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;

XX vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;

XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX age-related macular degeneration; arterial restenosis; angina;

XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

XX wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PF 23-JUN-2000; 2000US-0213637P.

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PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0223695P.
PR 17-AUG-2000; 2000US-00643557.
PR 23-AUG-2000; 2000WO-US023352.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen MB, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX NPI; 2002-090516/12.
XX N-PSDB; ABL88202.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 262; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The PRO polynucleotides have applications in molecular biology,
XX including use as hybridisation probes, and in chromosome and gene
XX mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX exemplification of the present invention
XX
XX Sequence 310 AA;
XX
XX Query Match 100.0%; Score 310; DB 5; Length 310;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-295;
XX Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MALRRPRLRLCARLPDPFLLFRGCLIGAVNLKSSNRTFVQBFESVELSCIITDSQT 60
|||||
```


CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG6326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCLITDSQT 60
Db 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCLITDSQT 60

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Db 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKINWVTRDSALYRCEVVAR 120

Qy 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHYSWYRNDVPL 180

Qy 181 PTDSTRANPRFNSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEYVDL 240
Db 181 PTDSTRANPRFNSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEYVDL 240

Qy 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKXPKGPDGVNYIRTDDEG 300
Db 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKXPKGPDGVNYIRTDDEG 300

Qy 301 DFRKSSFVI 310
Db 301 DFRKSSFVI 310

RESULT 15
ABG65296
ID ABG65296 standard; protein; 310 AA.
XX
AC ABG65296;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human albumin fusion protein #1971.
XX
KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytostatic; antifertility; antinflammatory; antiulcer;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177137-A1.
XX
PD 18-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011988.
XX
PR 12-APR-2000; 2000US-0229358P.
PR 25-APR-2000; 2000US-0199384P.
PR 21-DEC-2000; 2000US-0256931P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Haseltine WA;

XX WPI; 2002-010886/01.
DR
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein.
XX
PS Claim 1; Page 1893-1894; 2102pp; English.
XX
CC The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA), also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or disorder
CC that may be modulated by therapeutic protein X. The albumin extends the
CC shelf-life of protein X, and may increase its biological in vitro/in vivo
CC activity. The protein is useful for treating and diagnosing disorders
CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG6326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ Sequence 310 AA;

Query Match 100.0%; Score 310; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCLITDSQT 60
Db 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCLITDSQT 60

Qy 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKINWVTRDSALYRCEVVAR 120
Db 61 SDPRIWKKIODEQTTVFFDNKIQGLAGRAEILGKTSKINWVTRDSALYRCEVVAR 120

Qy 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQVKPTVPCRVKAVPVGKMATLHCQESGHPHYSWYRNDVPL 180

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Db 181 PTDSTRANPRFNSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEYVDL 240

Qy 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKXPKGPDGVNYIRTDDEG 300
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Qy 301 DFRKSSFVI 310
Db 301 DFRKSSFVI 310

Search completed: June 15, 2004, 11:09:57
Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:08:05 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531C-15

Perfect score: 310

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	310	100.0	310	4	US-09-905-125A-423
3	310	100.0	310	4	US-09-902-775A-423
4	7	2.3	14	2	US-08-310-912A-190
5	7	2.3	14	3	US-09-301-085-190
6	7	2.3	14	5	PCT-US95-04589-190
7	7	2.3	52	3	US-09-330-330-9
8	7	2.3	119	4	US-09-134-001C-5228
9	7	2.3	148	4	US-09-489-039A-14211
10	7	2.3	215	4	US-09-328-352-6750
11	7	2.3	220	4	US-09-134-000C-6778
12	7	2.3	223	4	US-09-252-991A-32267
13	7	2.3	224	4	US-09-252-991A-24969
14	7	2.3	240	4	US-09-252-991A-17237
15	7	2.3	241	1	US-08-484-272-2
16	7	2.3	241	1	US-08-476-489-2
17	7	2.3	241	1	US-08-467-070-2
18	7	2.3	241	1	US-08-467-070A-2
19	7	2.3	241	5	PCT-US91-11669-2
20	7	2.3	244	3	US-08-883-086-9
21	7	2.3	244	4	US-09-589-287B-5
22	7	2.3	244	4	US-09-588-947A-5
23	7	2.3	244	4	US-09-131-237C-5
24	7	2.3	244	4	US-09-589-286A-5
25	7	2.3	249	2	US-09-154-802-1
26	7	2.3	249	3	US-09-373-029-1
27	7	2.3	325	4	US-09-252-991A-31408

ALIGNMENTS

RESULT 1

US-09-907-794A-423
Sequence 423, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pao, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Sequence 4, Appli
Sequence 16, Appl
Sequence 172, App
Sequence 11, Appl
Sequence 28162, A
Sequence 8, Appli
Sequence 19322, A
Sequence 12, Appl
Sequence 18576, A
Sequence 18110, A
Sequence 25264, A
Sequence 19749, A
Sequence 2, Appli
Sequence 3, Appli
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl

;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
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;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.4e-279;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQBFESVELSCIITDSQT 60
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Qy 61 SDPRIEMKKIQDEQTYTVPFDNKIQDLAGRAEILGKTSLKINVTTRDSALYRCVVAR 120
Db 61 SDPRIEMKKIQDEQTYTVPFDNKIQDLAGRAEILGKTSLKINVTTRDSALYRCVVAR 120

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Db 121 NDRKEIDEIVIELTVQVKPVTVPVCRVPAVPVGVKMATLHCQSEGHPRPHYSWYRNDVPL 180

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Db 181 PTDSRANPRFRNSSPHLSETGTLVFTAVHKDDSGQYCIANDAGSARCEQEVEYDL 240

Qy 241 NIGGIIGVVLVAVLALITIGCCAYRGGYFINKKQDGESYKNPKGPDGVNYIETDRBG 300
Db 241 NIGGIIGVVLVAVLALITIGCCAYRGGYFINKKQDGESYKNPKGPDGVNYIETDRBG 300

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Db 301 DFRHKSFFVI 310

RESULT 2

US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,125A
;; PRIOR FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
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;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
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;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-905-125A-423

Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.4e-279;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQBFESVELSCIITDSQT 60
Db 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQBFESVELSCIITDSQT 60

Qy 61 SDPRIEMKKIQDEQTYTVPFDNKIQDLAGRAEILGKTSLKINVTTRDSALYRCVVAR 120
Db 61 SDPRIEMKKIQDEQTYTVPFDNKIQDLAGRAEILGKTSLKINVTTRDSALYRCVVAR 120

Qy 121 NDRKEIDEIVIELTVQVKPVTVPVCRVPAVPVGVKMATLHCQSEGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQVKPVTVPVCRVPAVPVGVKMATLHCQSEGHPRPHYSWYRNDVPL 180

SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,912A
FILING DATE: September 22, 1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-310-912A-190

Query Match 2.3%; Score 7; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 LALITLG 262
|||||
DB 5 LALITLG 11

RESULT 5
US-09-301-085-190
Sequence 190, Application US/09301085
Patent No. 6262248
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/301,085
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1994-09-22
EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 190
LENGTH: 14
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-301-085-190

Query Match 2.3%; Score 7; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 LALITLG 262
|||||
DB 5 LALITLG 11

RESULT 6

PCT-US95-04589-190
Sequence 190, Application PC/TUS9504589
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04589-190
Query Match 2.3%; Score 7; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 256 LALITLG 262
|||||
DB 5 LALITLG 11
RESULT 7
US-09-330-330-9
Sequence 9, Application US/09330330
Patent No. 6274789
GENERAL INFORMATION:
APPLICANT: Yano, Masahiro
APPLICANT: Imamoto, Masao
APPLICANT: Katayose, Yuichi
APPLICANT: Sasaki, Takuji
APPLICANT: Wang, Zi-Xuan
APPLICANT: Yamanouchi, Utako
APPLICANT: Ishimaru, Lisa
TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/330.330
FILING DATE: 11-JUN-1999
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 10-181455
FILING DATE: 12-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-330-330-9

Query Match 2.3%; Score 7; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 LALITLG 262
|||||
Db 37 LALITLG 43

RESULT 8
US-09-134-001C-5228
Sequence 5228, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134.001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5228
LENGTH: 119
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5228

Query Match 2.3%; Score 7; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VVLAVLA 257
|||||
Db 48 VVLAVLA 54

RESULT 9
US-09-489-039A-14211

Sequence 14211, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489.039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14211
LENGTH: 148
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14211

Query Match 2.3%; Score 7; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 253 LAVLALI 259
|||||
Db 89 LAVLALI 95

RESULT 10
US-09-328-352-6750
Sequence 6750, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328.352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6750
LENGTH: 215
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-6750

Query Match 2.3%; Score 7; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 GGIIGGV 249
|||||
Db 100 GGIIGGV 106

RESULT 11
US-09-134-000C-6778
Sequence 6778, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134.000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6778
LENGTH: 220
TYPE: PRT
ORGANISM: Enterococcus faecalis

US-09-134-000C-6778

Query Match 2.3%; Score 7; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 GGIIIGV 249
|||||||
DB 50 GGIIIGV 56

RESULT 12

US-09-252-991A-32267
; Sequence 32267, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32267
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32267

Query Match 2.3%; Score 7; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RRPPRLR 10
|||||||
DB 5 RRPPRLR 11

RESULT 13

US-09-252-991A-24969
; Sequence 24969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24969
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24969

Query Match 2.3%; Score 7; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RRPPRLR 10
|||||||
DB 44 RRPPRLR 50

RESULT 14

US-09-252-991A-17237
; Sequence 17237, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17237
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17237

Query Match 2.3%; Score 7; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RRPPRLR 10
|||||||
DB 191 RRPPRLR 197

RESULT 15

US-08-484-272-2
; Sequence 2, Application US/08484272
; Patent No. 5661004
; GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey
; APPLICANT: WARE, Carl
; TITLE OF INVENTION: LYMPHOTOXIN-BETA, LYMPHOTOXIN-BETA
; TITLE OF INVENTION: COMPLEXES, PHARMACEUTICAL PREPARATIONS AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,272
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/222,614
FILING DATE:
APPLICATION NUMBER: PCT/US91/04588
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/544,862
FILING DATE: 27-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James P.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B129C1P11
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090

```

; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-272-2

Query Match      2.3%; Score 7; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      252 VLAVLAL 258
          |||||
Db      37  VLAVLAL 43

```

Search completed: June 15, 2004, 11:13:23
Job time : 17.5 secs

APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-423

Query Match 100.0%; Score 310; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLDPDFLLLLFRGCLIGAVNLKSSNRTPVQEFESVELSCIITDSOT 60
DB 1 MALRRPRLRLCARLDPDFLLLLFRGCLIGAVNLKSSNRTPVQEFESVELSCIITDSOT 60
QY 61 SDPRIWKIKIQEQTYYVFDNKKIQGLAGRAEILGKTSLKINVTTRDSALYRCVVAR 120
DB 61 SDPRIWKIKIQEQTYYVFDNKKIQGLAGRAEILGKTSLKINVTTRDSALYRCVVAR 120
QY 121 NDRKEIDEIVLTQVKFVTPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVLTQVKFVTPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFSSFLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEVEYDL 240
DB 181 PTDSRANPRFSSFLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEVEYDL 240
QY 241 NIGGIIGVVLAVLALITLIGCCAYRRGYFINNKQGESYKNPKGPDGVNVRTDEG 300
DB 241 NIGGIIGVVLAVLALITLIGCCAYRRGYFINNKQGESYKNPKGPDGVNVRTDEG 300
QY 301 DFRHKSSPVI 310
DB 301 DFRHKSSPVI 310

RESULT 2
US-09-909-088B-423
Sequence 423, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.

Query Match 100.0%; Score 310; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-824-423

Query Match 100.0%; Score 310; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293; Mismatches 0; Indels 0; Gaps 0;
Matches 310; Conservative 0;

Qy 1 MALRPPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQBFESVLSLTIIDTSQT 60
Db 1 MALRPPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQBFESVLSLTIIDTSQT 60

Qy 61 SDPRIWKKIODEQTTVFFDNKIQDLAGRAEILGKTSLKIMNVRTDSALYRCEVVAR 120
Db 61 SDPRIWKKIODEQTTVFFDNKIQDLAGRAEILGKTSLKIMNVRTDSALYRCEVVAR 120

Qy 121 NDRKEIDSVIELTVQVKPTVPCRVKAVPVGMATLHCQESGHPHYSWYRNDVPL 180
Db 121 NDRKEIDSVIELTVQVKPTVPCRVKAVPVGMATLHCQESGHPHYSWYRNDVPL 180

Qy 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEVEYDL 240
Db 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEVEYDL 240

Qy 241 NIGGIIGVLVLAVALITIGICCAVRGYPFINNKQGESYKPKGPDGVNVRTDEEG 300
Db 241 NIGGIIGVLVLAVALITIGICCAVRGYPFINNKQGESYKPKGPDGVNVRTDEEG 300

Qy 301 DFRHKSFPVI 310
Db 301 DFRHKSFPVI 310

RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavina, Ivar J.

;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/907,841
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 423
;; LENGTH: 310
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-841-423

Query Match 100.0%; Score 310; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293; Mismatches 0; Indels 0; Gaps 0;
Matches 310; Conservative 0;

Qy 1 MALRPPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQBFESVLSLTIIDTSQT 60
Db 1 MALRPPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTPVQBFESVLSLTIIDTSQT 60

Qy 61 SDPRIWKKIODEQTTVFFDNKIQDLAGRAEILGKTSLKIMNVRTDSALYRCEVVAR 120
Db 61 SDPRIWKKIODEQTTVFFDNKIQDLAGRAEILGKTSLKIMNVRTDSALYRCEVVAR 120

Qy 121 NDRKEIDSVIELTVQVKPTVPCRVKAVPVGMATLHCQESGHPHYSWYRNDVPL 180
Db 121 NDRKEIDSVIELTVQVKPTVPCRVKAVPVGMATLHCQESGHPHYSWYRNDVPL 180

Qy 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEVEYDL 240
Db 181 PTDSRANPRFNSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQEVEYDL 240

Qy 241 NIGGIIGVLVLAVALITIGICCAVRGYPFINNKQGESYKPKGPDGVNVRTDEEG 300
Db 241 NIGGIIGVLVLAVALITIGICCAVRGYPFINNKQGESYKPKGPDGVNVRTDEEG 300

Qy 301 DFRHKSFPVI 310
Db 301 DFRHKSFPVI 310

RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011

Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/004,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien

US-09-904-011-423
Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRPRLRLCARLPDPFLLALLFRGCLIGAVNLKSSNRTTPVVOBFESVLSCLITDSQT 60
DB 1 MALRRPRLRLCARLPDPFLLALLFRGCLIGAVNLKSSNRTTPVVOBFESVLSCLITDSQT 60
QY 61 SDPRIEMKKIQDBQTTTYVFFDNKIQDLAGRAELIGKTSLKIMNVTTRDSALYRCEVVAR 120
DB 61 SDPRIEMKKIQDBQTTTYVFFDNKIQDLAGRAELIGKTSLKIMNVTTRDSALYRCEVVAR 120
QY 121 NDRKEIDBIIVHLTVQVKPTVPCRVKAPVPGVGMATLHCQSESEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDBIIVHLTVQVKPTVPCRVKAPVPGVGMATLHCQSESEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEYVDL 240
DB 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEYVDL 240
QY 241 NIGGIIGVVLVAVLALITLIGICCAAYRRGYFINNKQDGESYKNPGKPDGWNVYRTDDEG 300
DB 241 NIGGIIGVVLVAVLALITLIGICCAAYRRGYFINNKQDGESYKNPGKPDGWNVYRTDDEG 300
QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310
RESULT 8
US-09-906-742-423
Sequence 423, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698

APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAURPPRLRLCARLPDFLLLPGRGLIGAVNLKSNRTPVQEFESVLSCLITDSQT 60
Db 1 MAURPPRLRLCARLPDFLLLPGRGLIGAVNLKSNRTPVQEFESVLSCLITDSQT 60
Qy 61 SDPIEWKKIQDQTTTVPFDNKIQDGLAGRAELTGKTSLKINWVTRDSALYCEVVAR 120
Db 61 SDPIEWKKIQDQTTTVPFDNKIQDGLAGRAELTGKTSLKINWVTRDSALYCEVVAR 120
Qy 121 NDRKEIDEIVIELTVQKPTVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQKPTVPCRVKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
Qy 181 PTDSRANPRFNSFHLNSTGTAVTAVHKDQSGQYTCASNDAGSARCBEBMEVYDL 240
Db 181 PTDSRANPRFNSFHLNSTGTAVTAVHKDQSGQYTCASNDAGSARCBEBMEVYDL 240
Qy 241 NIGGIGGVLVAVLALITLIGCCAYRRGYFINNKDGHGYKXNPKPGDGVNIRTDEEG 300
Db 241 NIGGIGGVLVAVLALITLIGCCAYRRGYFINNKDGHGYKXNPKPGDGVNIRTDEEG 300
Qy 301 DFRHKSFSVI 310
Db 301 DFRHKSFSVI 310

RESULT 9
US-09-906-838-423
Sequence 423, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCTIITDSQT 60
Db 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCTIITDSQT 60
Qy 61 SDPRIWKKIODEQTYTTFDNNKIQDLAGRAEIIIGKTSKIMNVTTRDSALYRCVVAR 120
Db 61 SDPRIWKKIODEQTYTTFDNNKIQDLAGRAEIIIGKTSKIMNVTTRDSALYRCVVAR 120
Qy 121 NDRKEIDEIVELTVQVKPVTVCVPRKAVPVGKMATLHCQSEGHGPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVELTVQVKPVTVCVPRKAVPVGKMATLHCQSEGHGPHYSWYRNDVPL 180
Qy 181 PTDSRANPRFRNSSPHLNSCTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
Db 181 PTDSRANPRFRNSSPHLNSCTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
Qy 241 NIGGIIGGVVAVLALITIGICAYRRGYFINNKQDGESYKNPKGPDGVNVIITDEEG 300
Db 241 NIGGIIGGVVAVLALITIGICAYRRGYFINNKQDGESYKNPKGPDGVNVIITDEEG 300
Qy 301 DFRHKSSSVFI 310
Db 301 DFRHKSSSVFI 310
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RESULT 10

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US-09-907-613-423
; Sequence 423, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottstein, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9,8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCTIITDSQT 60
Db 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVQEFSEVLSCTIITDSQT 60
Qy 61 SDPRIWKKIODEQTYTTFDNNKIQDLAGRAEIIIGKTSKIMNVTTRDSALYRCVVAR 120
Db 61 SDPRIWKKIODEQTYTTFDNNKIQDLAGRAEIIIGKTSKIMNVTTRDSALYRCVVAR 120
Qy 121 NDRKEIDEIVELTVQVKPVTVCVPRKAVPVGKMATLHCQSEGHGPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVELTVQVKPVTVCVPRKAVPVGKMATLHCQSEGHGPHYSWYRNDVPL 180
Qy 181 PTDSRANPRFRNSSPHLNSCTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
Db 181 PTDSRANPRFRNSSPHLNSCTGLVFTAVHKDDSGQYTCIASNDAGSARCEQMEVYDL 240
Qy 241 NIGGIIGGVVAVLALITIGICAYRRGYFINNKQDGESYKNPKGPDGVNVIITDEEG 300
Db 241 NIGGIIGGVVAVLALITIGICAYRRGYFINNKQDGESYKNPKGPDGVNVIITDEEG 300
Qy 301 DFRHKSSSVFI 310
Db 301 DFRHKSSSVFI 310
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RESULT 11

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US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
```

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-942-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSSNRTPVVOEFESVLSCLITDSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLRGCLIGAVNLKSSNRTPVVOEFESVLSCLITDSQT 60
QY 61 SDPRIWKKIQDEQTTVFFDNKIQGLAGRAEILGKTSKIMNVTDRDSALYRCVVAR 120
DB 61 SDPRIWKKIQDEQTTVFFDNKIQGLAGRAEILGKTSKIMNVTDRDSALYRCVVAR 120

QY 121 NDRKEIDEIVIELTVQVKPVPVCRVDPKAVPVGKMATLHCOESRHHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPVPVCRVDPKAVPVGKMATLHCOESRHHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSFHLNSETGLVFTAVHKDSDGGQYYCIASNDAGSARCEEQMEVYDL 240
DB 181 PTDSRANPRFRNSSFHLNSETGLVFTAVHKDSDGGQYYCIASNDAGSARCEEQMEVYDL 240
QY 241 NIGGIIGGVLVLAVALIALITGLICCCAYRRGVFFINNKODGESYKPKPGDGNYIRTDBEG 300
DB 241 NIGGIIGGVLVLAVALIALITGLICCCAYRRGVFFINNKODGESYKPKPGDGNYIRTDBEG 300
QY 301 DFRHKSSPVI 310
DB 301 DFRHKSSPVI 310

RESULT 12
US-09-904-859-423
Sequence 423, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214


```
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-504-859-423

Query Match      100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBPESVELSCIITDSQT 60
DB 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBPESVELSCIITDSQT 60

QY 61 SDPRIEMKKIQDEQTYTTFDFNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120
DB 61 SDPRIEMKKIQDEQTYTTFDFNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120

QY 121 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYTCIASNDAGSARCEQEVEYDL 240
DB 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYTCIASNDAGSARCEQEVEYDL 240

QY 241 NGGGIIGVVLAVLALITLGGICAYRRGYFINNKQDGESYKNPKGPDGVNVRTDBEG 300
DB 241 NGGGIIGVVLAVLALITLGGICAYRRGYFINNKQDGESYKNPKGPDGVNVRTDBEG 300

QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310
```

RESULT 13
US-09-909-204-423

Sequence 423, Application US/09909204
Publication No. US20030036061A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.

```
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-204-423
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Query Match 100.0%; Score 310; DB 10; Length 310;

Best Local Similarity 100.0%; Pred. No. 9.8e-293;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBPESVELSCIITDSQT 60

DB 1 MALRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQBPESVELSCIITDSQT 60

QY 61 SDPRIEMKKIQDEQTYTTFDFNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120

DB 61 SDPRIEMKKIQDEQTYTTFDFNKKIQDLAGRAEILGKTSKIWNVTRDSALYRCVAVAR 120

QY 121 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

DB 121 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYTCIASNDAGSARCEQEVEYDL 240

DB 181 PTDSRANPRFRNSSPHLNSSETGLVFTAVHKDDSGQYTCIASNDAGSARCEQEVEYDL 240

Qy 241 NIGGIIGVLVWLVAVLALITLIGICCAVRGYFFINNKQDGSYKPNKPGKPDGVNYIRTDREG 300
Db 241 NIGGIIGVLVWLVAVLALITLIGICCAVRGYFFINNKQDGSYKPNKPGKPDGVNYIRTDREG 300
Qy 301 DFRHKSFSVI 310
Db 301 DFRHKSFSVI 310

RESULT 14

US-09-904-820-423
; Sequence 423, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904, 820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-820-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALRRPRLRLCARLPDFFLLLPRLGCLIGAVNLKSSNRTFVQBFESVLSCTITDSQT 60
Db 1 MALRRPRLRLCARLPDFFLLLPRLGCLIGAVNLKSSNRTFVQBFESVLSCTITDSQT 60
Qy 61 SDPRIEMKKIQDEQTTVFVDNKIQGLAGRAEILGKTSLSKIMNVRDLSALYRCEVVAR 120
Db 61 SDPRIEMKKIQDEQTTVFVDNKIQGLAGRAEILGKTSLSKIMNVRDLSALYRCEVVAR 120
Qy 121 NDRKEIDEIVIELTVQVKPVPVCRKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
Db 121 NDRKEIDEIVIELTVQVKPVPVCRKAVPVGKMATLHCQESGHPRPHYSWYRNDVPL 180
Qy 181 PTDSRANPRFRNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQMEVYDL 240
Db 181 PTDSRANPRFRNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEQMEVYDL 240
Qy 241 NIGGIIGVLVWLVAVLALITLIGICCAVRGYFFINNKQDGSYKPNKPGKPDGVNYIRTDREG 300
Db 241 NIGGIIGVLVWLVAVLALITLIGICCAVRGYFFINNKQDGSYKPNKPGKPDGVNYIRTDREG 300
Qy 301 DFRHKSFSVI 310
Db 301 DFRHKSFSVI 310

RESULT 15

US-09-904-786-423
; Sequence 423, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,786
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-786-423

Query Match 100.0%; Score 310; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQEFSELSCTIITDSQT 60
Db 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTVPVQEFSELSCTIITDSQT 60

QY 61 SDPRLEWKKIQDEQTTTTFDNNKIQGDLAGRAEILGKTSLKWNVTRRDSALYRCEVVAR 120
Db 61 SDPRLEWKKIQDEQTTTTFDNNKIQGDLAGRAEILGKTSLKWNVTRRDSALYRCEVVAR 120

QY 121 NDRKEIDEIVIELTVQVKPVTVCVRPKAVPVGKMATLHCQESBEGHPRPHYSWYRNDVFL 180
Db 121 NDRKEIDEIVIELTVQVKPVTVCVRPKAVPVGKMATLHCQESBEGHPRPHYSWYRNDVFL 180

QY 181 PTDSRANPRFRNSSPHLNSETGTLVFTAVHKDDSGQYCIASNDAGSARCEQEWEVYDL 240
Db 181 PTDSRANPRFRNSSPHLNSETGTLVFTAVHKDDSGQYCIASNDAGSARCEQEWEVYDL 240

QY 241 NIGGIIGGVLVLAVALITLGCAYRGGYFINNKQGESYKNPKGPDGVNYIRTDREG 300
Db 241 NIGGIIGGVLVLAVALITLGCAYRGGYFINNKQGESYKNPKGPDGVNYIRTDREG 300

QY 301 DFRHKSSFVI 310
Db 301 DFRHKSSFVI 310

Search completed: June 15, 2004, 11:14:53
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:06:35 ; Search time 14 Seconds
(without alignments)
2129.955 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPRLRLCARLPDFL.....VNYIRTBGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78.*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.6	290	2 168750	MHC class I lympho
2	8	2.6	336	2 A86406	probable RING zinc
3	8	2.6	342	1 HLHUC4	MHC class I histoc
4	8	2.6	348	2 E82933	type I restriction
5	8	2.6	366	2 JH0546	class I histocompa
6	8	2.6	366	2 JH0547	class I histocompa
7	8	2.6	366	2 JH0545	class I histocompa
8	8	2.6	492	2 I37078	HLA-C alpha chain
9	8	2.6	492	2 AB1013	probable membrane
10	8	2.6	784	2 A86676	carbon starvation
11	7	2.3	77	2 JC5645	lymphotoxin beta -
12	7	2.3	113	2 AH1748	hypothetical prote
13	7	2.3	171	2 G70548	hypothetical prote
14	7	2.3	172	2 T08548	hypothetical prote
15	7	2.3	173	2 T01282	hypothetical prote
16	7	2.3	173	2 B90241	hypothetical prote
17	7	2.3	173	2 T25730	hypothetical prote
18	7	2.3	177	2 B85938	partial probable s
19	7	2.3	177	2 B90988	cobalt transport p
20	7	2.3	208	2 T03627	GTP-binding protei
21	7	2.3	208	2 T01598	GTP-binding protei
22	7	2.3	211	2 B86888	hypothetical prote
23	7	2.3	214	2 T47268	phosphatidylserine
24	7	2.3	217	2 T30446	occlusion-derived
25	7	2.3	242	2 G84315	hypothetical prote
26	7	2.3	244	2 A46066	lymphotoxin beta -
27	7	2.3	255	2 T35883	transcription regu
28	7	2.3	280	2 PH0269	epidermal autoanti
29	7	2.3	284	2 B84023	phosphate ABC tran

30 7 2.3 297 2 AB3037 hypothetical prote
31 7 2.3 297 2 A81002 conserved hypothet
32 7 2.3 299 2 A98249 nitrate transport
33 7 2.3 300 2 A82017 probable lipoprote
34 7 2.3 302 2 B70471 heat shock protein
35 7 2.3 306 2 I49139 lymphotoxin-beta -
36 7 2.3 314 2 AG3093 hypothetical prote
37 7 2.3 314 2 C98193 sugar transport sy
38 7 2.3 324 2 T27302 hypothetical prote
39 7 2.3 333 2 I38974 G protein-coupled
40 7 2.3 343 2 H95879 probable sugar ABC
41 7 2.3 346 2 D75303 conserved hypothet
42 7 2.3 362 2 G75614 G3BP family prote
43 7 2.3 375 2 T46378 hypothetical prote
44 7 2.3 376 2 F71815 hypothetical prote
45 7 2.3 380 2 B88421 protein R74.2 [imp

ALIGNMENTS

RESULT 1

168750 MHC class I lymphocyte antigen - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000

C/Accession: I68750

R/Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, B.H.

Immunogenetics 29, 297-307, 1989

A/Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B

A/Reference number: I54457; MUID:89233295; PMID:2714852

A/Accession: I68750

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-290 <RES>

A/Cross-references: GB:W28207; NID:G576478; PIDN:APA53259.1; PID:G576479

C/Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:144-209/domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256

Db 241 VLVVLAVL 248

RESULT 2

A86406

probable RING zinc finger protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: A86406

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: A86406

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-336 <STO>

A/Cross-references: GB:AE005172; NID:g11024872; PIDN:AAAG26956.1; GSPDB:GN00141

C/Genetics:

A/Map position: 1

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Query Match      2.6%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      250 LVVLAVLA 257
DB      28 LVVLAVLA 35
|||||

RESULT 3
HLHUC4
MHC class I histocompatibility antigen HLA-C4 alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C:Accession: A24512
R:Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
A:Title: Comparison of HLA Class I gene sequences. Derivation of locus-specific oligonucleotide probes for the A, B, and C loci.
A:Reference number: A92500; MUID:86033791; PMID:3863816
A:Accession: A24512
A:Molecule type: DNA
A:Residues: 1-342 <DAV>
A:Cross-references: GB:M11886; NID:q184173; PIDN:AAAS2665.1; PID:g386777
C:Genetics:
A:Gene: GDB:HLA-C
A:Cross-references: GDB:119311; OMIM:142840
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F:196-261/Domain: immunoglobulin homology <IMM>
F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      2.6%; Score 8; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      249 VLVVLAVL 256
DB      293 VLVVLAVL 300
|||||

RESULT 4
B82933
type I restriction enzyme M protein, truncated homolog UU098 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Oct-2002
C:Accession: B82933
R:Glaas, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mirror image of the complete sequence of Ureaplasma urealyticum.
A:Reference number: A82870
A:Accession: B82933
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <GLA>
A:Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30504.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: hsdM-1; UU098
A:Genetic code: SG3
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match      2.6%; Score 8; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      123 RKEIDEIV 130
DB      336 RKEIDEIV 343
|||||

RESULT 5
JH0546
Class I histocompatibility antigen Gogo-C0201 heavy chain precursor - lowland gorilla

```

```

class I histocompatibility antigen Gogo-C0202 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0546
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A:Reference number: JH0534; MUID:92078860; PMID:1744581
A:Accession: JH0546
A:Molecule type: DNA
A:Residues: 1-366 <LAW>
A:Cross-references: EMBL:X60249; NID:g22882; PIDN:CRA42801.1; PID:g22883
A:Experimental source: EBV-transformed B cell
C:Genetics:
A:Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
P:1-24/Domain: signal sequence #status predicted <SIG>
P:25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0202 #status p;
P:115-206/Domain: alpha-1 <AL1>
P:220-285/Domain: immunoglobulin homology <IMM>
P:299-366/Domain: intracellular #status predicted <INT>

Query Match      2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      249 VLVVLAVL 256
DB      317 VLVVLAVL 324
|||||

RESULT 6
JH0547
class I histocompatibility antigen Gogo-C0203 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0547
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A:Reference number: JH0534; MUID:92078860; PMID:1744581
A:Accession: JH0547
A:Molecule type: DNA
A:Residues: 1-366 <LAW>
A:Cross-references: EMBL:X60248; NID:g22884; PIDN:CRA42800.1; PID:g22885
A:Experimental source: EBV-transformed B cell
C:Genetics:
A:Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
P:1-24/Domain: signal sequence #status predicted <SIG>
P:25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0203 #status p;
P:115-206/Domain: alpha-1 <AL1>
P:220-285/Domain: immunoglobulin homology <IMM>
P:299-366/Domain: intracellular #status predicted <INT>

Query Match      2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      249 VLVVLAVL 256
DB      317 VLVVLAVL 324
|||||

RESULT 7
JH0545
Class I histocompatibility antigen Gogo-C0201 heavy chain precursor - lowland gorilla

```

C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0545
R;Lawlor, D.A.; Warren, B.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A;Reference number: JH0534; MUID:92078860; PMID:1744581
A;Accession: JH0545
A;Molecule type: DNA
A;Residues: 1-366 <LAW>
A;Cross-references: EMBL:X60251; NID:g22880; PIDN:CAA42803.1; PID:g22881
A;Experimental source: EBV-transformed B cell
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
P;1-24/Domain: signal sequence #status predicted <SIG>
P;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0201 #status pre
P;25-114/Domain: alpha-1 <AL1>
P;115-206/Domain: alpha-2 <AL2>
P;207-298/Domain: alpha-3 <AL3>
P;220-285/Domain: immunoglobulin homology <IMM>
P;299-366/Domain: intracellular #status predicted <INT>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.1; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 249 VLVLAVL 256
| | | | |
Db 317 VLVLAVL 324

RESULT 8
I37078
HLA-C alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I37078
R;Vilches, C.; Bunce, M.; de Pablo, R.; Herrero, M.J.; Kreisler, M.
Tissue Antigens 46, 19-23, 1995
A;Title: Anchored PCR cloning of the novel HLA-Cw*0704 allele detected by PCR-SSP.
A;Reference number: I37078; MUID:96086482; PMID:7482492
A;Accession: I37078
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-366 <RES>
A;Cross-references: EMBL:X83394; NID:g669131; PIDN:CAA58313.1; PID:g669132
C;Genetics:
A;Gene: Cw*0704
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
P;220-285/Domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.1; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 249 VLVLAVL 256
| | | | |
Db 317 VLVLAVL 324

RESULT 9
AB1013
probable membrane protein STY4415 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB1013
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB1013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-492 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09203.1; PID:g16505207; GSPDB:GN00176
C;Genetics:
A;Gene: STY4415

Query Match 2.6%; Score 8; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 9.2; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 242 IGGIIGGV 249
| | | | |
Db 244 IGGIIGGV 251

RESULT 10
AB6676
carbon starvation protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: AB6676
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrh
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: AB6625; MUID:21235186; PMID:11337471
A;Accession: AB6676
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-784 <STO>
A;Cross-references: GB:AB005176; PID:g12723283; PIDN:AAK04507.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: CstA
C;Superfamily: carbon starvation protein

Query Match 2.6%; Score 8; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 14; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 252 VLAVLALI 259
| | | | |
Db 223 VLAVLALI 230

RESULT 11
JC5645
lymphotoxin beta - human
N;Alternate names: non-Hodgkin's lymphoma
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 05-Nov-1999
C;Accession: JC5645
R;Warzocha, K.; Renard, N.; Charlot, C.; Bienvenu, J.; Coiffier, B.; Salles, G.
Biochem. Biophys. Res. Commun. 238, 273-276, 1997
A;Title: Identification of two lymphotoxin beta isoforms expressed in human lymphoid ce
A;Reference number: JC5645; MUID:97445965; PMID:9299492
A;Accession: JC5645
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-77 <WAR>
A;Cross-references: GB:U89922; NID:g1870795; PIDN:AAC51769.1; PID:g1870796
C;Comment: This protein is involved in the development and function of the immune syste

Query Match 2.3%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 252 VLAVLALI 258
| | | | |

Db 40 VLAVLAL 46

RESULT 12
AH1748
hypothetical protein lin2533 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AH1748
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1748
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97760.1; PID:g16415055; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2533

Query Match 2.3%; Score 7; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 GGIIGGV 249
|||||
DB 15 GGIIGGV 21

RESULT 13
G70548
hypothetical protein Rv0556 - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
C:Accession: G70548
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70548
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-171 <COL>
A:Cross-references: GB:Z95558; GB:AL123456; NID:G3261781; PIDN:CAB08967.1; PID:e316801;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0556
C:Superfamily: *Mycobacterium tuberculosis* hypothetical protein Rv0556

Query Match 2.3%; Score 7; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVL 256
|||||
DB 150 LVVLAVL 156

RESULT 14
T08548
hypothetical protein F27B13.110 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C:Accession: T08548

R:Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; M submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16442
A:Accession: T08548
A:Molecule type: DNA
A:Residues: 1-172 <BEV>
A:Cross-references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.110
A:Experimental source: cultivar Columbia; BAC clone F27B13
C:Genetics:
A:Gene: ATSP:F27B13.110
A:Map position: 4

Query Match 2.3%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPPRLRL 11
|||||
DB 37 RPPRLRL 43

RESULT 15
T01282
hypothetical protein At2g19340 [imported] - *Arabidopsis thaliana*
N:Alternate names: hypothetical protein F27F23.14
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C:Accession: T01282; R84575
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Ka submitted to the EMBL Data Library, May 1998
A:Description: *Arabidopsis thaliana* chromosome II BAC F27F23 genomic sequence.
A:Reference number: Z14177
A:Accession: T01282
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-173 <ROU>
A:Cross-references: EMBL:AC003058; NID:g3135250; PID:g3135264
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: R84575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-173 <STO>
A:Cross-references: GB:AE002093; NID:g3135264; PIDN:AAC16464.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g19340; F27F23.14
A:Map position: 2

Query Match 2.3%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPPRLRL 11
|||||
DB 38 RPPRLRL 44

Search completed: June 15, 2004, 11:12:37
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:05:10 ; Search time 10 Seconds
(without alignments)
1614.175 Million cell updates/sec

Title: US-09-524-531c-15

Perfect score: 310

Sequence: 1 MALRRPRLRLCARLPDFL.....VNYRTDEGDFRHKGSFVI 310

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	8	2.6	80	1 TX3A_PHONI	P81793 pseudotria
2	8	2.6	366	1 IC02_GORGO	P30385 gorilla gor
3	8	2.6	366	1 IC03_GORGO	P30386 gorilla gor
4	8	2.6	366	1 IC04_GORGO	P30387 gorilla gor
5	8	2.6	366	1 IC07_HUMAN	P10321 homo sapien
6	8	2.6	366	1 IC18_HUMAN	Q29865 homo sapien
7	8	2.6	435	1 VG1K_SALTY	P40800 salmonella
8	7	2.3	161	1 TATB_STRCO	Q5fbr8 streptomyc
9	7	2.3	224	1 XLRI_MOUSE	Q92114 mus musculu
10	7	2.3	242	1 RS2_SHEON	Q8egh5 shewanella
11	7	2.3	244	1 TNFC_HUMAN	Q06643 homo sapien
12	7	2.3	244	1 TNFC_PANTR	Q86227 pan troglod
13	7	2.3	302	1 HTPX_AQUAE	O47798 aquifex aeo
14	7	2.3	306	1 TNFC_MOUSE	P41155 mus musculu
15	7	2.3	310	1 TNFC_HUMAN	Q9jml0 marmota mon
16	7	2.3	333	1 GPR8_HUMAN	P48146 homo sapien
17	7	2.3	343	1 HMD_METVO	Q50840 methanococ
18	7	2.3	374	1 TMI_SULTO	Q97149 eulobobus
19	7	2.3	403	1 TRP_ECOLI	P18199 escherichia
20	7	2.3	417	1 PVR_CERAE	P32506 cercopithec
21	7	2.3	417	1 PVR_HUMAN	P15151 homo sapien
22	7	2.3	418	1 SVTF_MOUSE	Q8c6n3 mus musculu
23	7	2.3	454	1 APY_SOLTU	P80595 solanum tub
24	7	2.3	481	1 LMR_A_STRLN	P46104 streptomyc
25	7	2.3	491	1 CPB4_RABIT	P00178 cryptolegus
26	7	2.3	491	1 CPB5_RABIT	P12789 oryctolegus
27	7	2.3	524	1 GTR2_HUMAN	P11168 homo sapien
28	7	2.3	574	1 IRL2_MOUSE	Q9ers7 mus musculu
29	7	2.3	595	1 IP2P_ARCFU	Q29490 archaeoglob
30	7	2.3	617	1 PYS1_PSERAE	Q06583 pseudomonas
31	7	2.3	643	1 S212_HUMAN	Q92959 homo sapien
32	7	2.3	643	1 S212_MOUSE	Q9epts5 mus musculu
33	7	2.3	643	1 S212_RAT	Q00910 rattus norv

RESULT 1
TX3A_PHONI STANDARD; PRT; 80 AA.

AC P81793;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neurotoxin Pn3A precursor.

OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phlebotominae.

OC NCEI_TaxID=6918;

RN NCEI_TaxID=6918;

RC TISSUE=Venom gland;

RP MEDLINE=99053416; PubMed=9839681;

RA Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.F.,

RA Cordeiro M.N., Diniz C.R., Romano-Silva M.A., Prado M.A.M.,

RA Gomez M.V., Beirao P.S.L.;

RT "Cloning, cDNA sequence analysis and patch clamp studies of a toxin

from the venom of the armed spider (Phlebotomina nigriventer).";

RL Toxicon 36:1971-1980(1998).

CC -1- FUNCTION: Antagonist of L-type calcium channels (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the spider toxin Tx3 family.

DR InterPro; IPR004169; spider toxin.

DR Pfam; PF02819; spider toxin; 1.

KW Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;

FT SIGNAL.

FT PROPEP.

FT CHAIN.

FT PROPEP.

FT SIGNAL.

FT PROPEP.

FT CHAIN.

FT PROPEP.

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FT CHAIN.

FT PROPEP.

FT SIGNAL.

ALIGNMENTS

34 7 2.3 688 1 PYS2_PSERAE Q06584 pseudomonas
35 7 2.3 693 1 NCPR_ASPNG Q00141 aspergillus
36 7 2.3 697 1 TGM2_CHICK Q01841 gallus gall
37 7 2.3 721 1 YJ1Y_ECOLI P39396 escherichia
38 7 2.3 729 1 GOA5_MOUSE Q9gye6 mus musculu
39 7 2.3 758 1 SC18_YEAST P18759 saccharomyc
40 7 2.3 840 1 CC16_YEAST P03798 saccharomyc
41 7 2.3 909 1 RPS2_ARATH Q42484 arabidopsis
42 7 2.3 981 1 SCA4_RICPE Q9aj37 rickettsia
43 7 2.3 987 1 K6P1_CANAL Q94201 candida alb
44 7 2.3 991 1 SCA4_RICSI Q9aj77 rickettsia
45 7 2.3 1011 1 SCA4_RICAP Q9aj83 rickettsia

Query Match 2.68; Score 8; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 LALITLGI 263

Db 12 LALITLGI 19

RESULT 2

1C02_GORGO STANDARD; PRT; 366 AA.

AC P30385;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 01-APR-1993 (Rel. 25, Last annotation update)

DE Class I histocompatibility antigen, GOGC-C0201 alpha chain precursor.

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Gorilla.


```

RT to human and chimpanzee class I.;
RL J. Exp. Med. 174:1491-1509(1991).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; J60248; CAA42800.1; -.
DR PIR; JH0547; JH0547.
DR HSSP; P30685; IABE.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 366
FT -----
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT GOGO-C0203 ALPHA CHAIN.
FT -----
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT TRANSMEM 333 366
FT DOMAIN 333 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT SEQUENCE 366 AA; 40970 MW; E8962C8189CNC001 CRC64;
FT -----
Query Match 2.6%; Score 8; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVLAVL 256
Db 317 VLVLAVL 324
|||||
|||||

RESULT 5
ID 1C07 HUMAN STANDARD; PRT; 366 AA.
AC P1321; O78061; Q29631; Q29652; Q29867; Q29990; Q95463;
AC Q95603; Q9MT31; Q9TP9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, CW-7 alpha chain precursor
DE (MHC class I antigen CW*7).
DE HLA-C OR HLAC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE OF 1-206 FROM N.A. (CW*0701).
RX MEDLINE=95176330; PubMed=7871529;
RA Steinle A., Schendel D.J.;
RT "HLA class I alleles of LCL 721 and 174xCEM.T2(T2).";

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RL Tissue Antigens 44:268-270(1994).
RN [2]
RP SEQUENCE OF 77-309 FROM N.A. (CW*0701).
RX MEDLINE=89233295; PubMed=2714852;
RA Pohla H., Kuon W., Tabaczewski P., Doerner C., Weiss E.H.;
RT "Allelic variation in HLA-B and HLA-C sequences and the evolution of
RT the HLA-B alleles.";
RL Immunogenetics 29:297-307(1989).
RN [3]
RP SEQUENCE OF 26-338 FROM N.A. (CW*0701).
RX MEDLINE=99416847; PubMed=10488744;
RA van der Vlies S.A., Voorter C.E., van den Berg-Loonen E.M.;
RT "There is more to HLA -C than exons 2 and 3: sequencing exons 1, 4 and
RT 5.";
RL Tissue Antigens 54:169-177(1999).
RN [4]
RP SEQUENCE FROM N.A. (CW*0702 AND CW*0704).
RX TISSUE=Blood;
RL MEDLINE=96232973; PubMed=8655361;
RA Wang H., Tokunaga K., Ishikawa Y., Asahina A., Kuwata S., Akaza T.,
RA Tadokoro K., Shibata Y., Takiguchi M., Juji T.;
RT "Identification and DNA typing of two Cw7 alleles (CW*0702 and
RT CW*0704) in Japanese, with the corrected sequence of CW*0702.";
RL Hum. Immunol. 45:52-58(1996).
RN [5]
RP SEQUENCE FROM N.A. (CW*0702).
RX MEDLINE=9809755; PubMed=9433339;
RA Cooper S.L., Adams E.J., Wells R.S., Walker C.M., Parham P.;
RT "A major histocompatibility complex class I allele shared by two
RT species of chimpanzee.";
RL Immunogenetics 47:212-217(1998).
RN [6]
RP SEQUENCE FROM N.A. (CW*0702 AND CW*0704).
RX TISSUE=Blood;
RL MEDLINE=22512041; PubMed=12622774;
RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.B., Parham P.,
RA Madrigal J.A., Little A.M.;
RT "Cloning and sequencing full-length HLA-B and -C genes.";
RL Tissue Antigens 61:20-48(2003).
RN [7]
RP SEQUENCE OF 25-366 FROM N.A. (CW*0703).
RX MEDLINE=8603791; PubMed=3863816;
RA Davidson W.F., Kress M., Khoury G., Jay G.;
RT "Comparison of HLA class I gene sequences. Derivation of
RT locus-specific oligonucleotide probes specific for HLA-A, HLA-B, and
RT HLA-C genes.";
RL J. Biol. Chem. 260:13414-13423(1985).
RN [8]
RP SEQUENCE FROM N.A. (CW*0704).
RX MEDLINE=96086482; PubMed=7482492;
RA Vilches C., Bunce M., de Pablo R., Herrero M.J., Kreisler M.;
RT "Anchored PCR cloning of the novel HLA-Cw*0704 allele detected by
RT PCR-SSP.";
RL Tissue Antigens 46:19-23(1995).
RN [9]
RP SEQUENCE FROM N.A. (CW*0704).
RX TISSUE=Melanoma;
RA Coulie P.G.;
RT "Identification of a new HLA-Cw7 allele.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A. (CW*0706).
RX MEDLINE=97161041; PubMed=9008313;
RA Vilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreisler M.;
RT "Molecular cloning of two new HLA-C alleles: CW*1801 and CW*0706.";
RL Tissue Antigens 48:698-702(1996).
RN [11]
RP SEQUENCE OF 26-206 FROM N.A. (CW*0709).
RX MEDLINE=98349393; PubMed=9686604;
RA Turner S., Ellexson M.B., Hickman H.D., Sidebottom D.A.,
RA Fernandez-Vina M., Confer D.L., Hildebrand W.H.;
RT "Sequence-based typing provides a new look at HLA-C diversity.";
RL J. Immunol. 161:1406-1413(1998).

```

RN SEQUENCE FROM N.A. (Cw*0711).
 RX MEDLINE=99299762; PubMed=10372547;
 RA Baurain J.-P., Coulie P.G.;
 RT "Correction of HLA-Cw*0501 and identification of HLA-Cw*0711.";
 RL Tissue Antigens 53:510-512(1999).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- POLYMORPHISM: The following alleles of Cw-7 are known: Cw*0701,
 CC Cw*0702, Cw*0703, Cw*0704, Cw*0706, Cw*0709 and Cw*0711. The
 CC sequence shown is that of Cw*0701.
 CC -----
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 CC -----
 DR EMBL; Z46810; CAA6840.1; -;
 DR EMBL; M28207; AAA53259.1; -;
 DR EMBL; Y18533; CAB71800.1; -;
 DR EMBL; Y18534; CAB71800.1; JOINED.
 DR EMBL; Y18535; CAB71800.1; JOINED.
 DR EMBL; Y18536; CAB71800.1; JOINED.
 DR EMBL; D38526; BAA07531.1; -;
 DR EMBL; D49819; BAA08625.1; -;
 DR EMBL; D49552; BAA08500.1; -;
 DR EMBL; AJ019177; CAA05125.1; ALT_SEQ.
 DR EMBL; AJ293016; CAC04321.1; -;
 DR EMBL; AJ293017; CAC04322.1; -;
 DR EMBL; AJ291815; CAC19191.1; -;
 DR EMBL; M11886; AAA52665.1; -;
 DR EMBL; X83394; CAA58313.1; -;
 DR EMBL; U09853; AAA50217.1; -;
 DR EMBL; X97321; CAA65986.1; -;
 DR EMBL; AF015557; AAC17722.1; -;
 DR EMBL; AF015556; AAC17722.1; JOINED.
 DR EMBL; AJ010749; CAA09341.1; -;
 DR PIR; A24512; HLHUC4.
 DR PIR; I37078; I37078.
 DR PIR; I37529; I37529.
 DR PIR; I68750; I68750.
 DR HSSP; P30460; IAGD.
 DR Genew; HGNC:4933; HLA-C.
 DR MIM; 142840; -;
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_1.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_1; 1.
 DR PRINTS; PR01638; MHCCLASS1.
 DR ProDom; PD000050; MHC_1; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 366
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT Cw-7 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206
 FT EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298
 FT EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308
 FT CONNECTING PEPTIDE.
 FT TRANSMEM 309 333
 FT CYTOPLASMIC TAIL.
 FT DOMAIN 334 366
 FT BY SIMILARITY.
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT BY SIMILARITY.

FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
 FT VARIANT 90 N -> K (in allele Cw*0702, allele
 FT Cw*1703, allele Cw*0704 and allele
 FT Cw*0711).
 FT /FTID=VAR 016590.
 FT S -> N (in allele Cw*0709).
 FT /FTID=VAR 016591.
 FT N -> K (in allele Cw*0709).
 FT /FTID=VAR 016592.
 FT L -> F (in allele Cw*0704 and allele
 FT Cw*0711).
 FT /FTID=VAR 016593.
 FT Y -> S (in allele Cw*0702 and allele
 FT Cw*0703).
 FT /FTID=VAR 016594.
 FT S -> F (in allele Cw*0704 and allele
 FT Cw*0711).
 FT /FTID=VAR 016595.
 FT L -> W (in allele Cw*0703).
 FT /FTID=VAR 016646.
 FT L -> D (in allele Cw*0704 and allele
 FT Cw*0711).
 FT /FTID=VAR 016596.
 FT T -> L (in allele Cw*0703).
 FT /FTID=VAR 016647.
 FT E -> K (in allele Cw*0704 and allele
 FT Cw*0711).
 FT /FTID=VAR 016597.
 FT M -> K (in allele Cw*0706).
 FT /FTID=VAR 016598.
 FT A -> V (in allele Cw*0706).
 FT /FTID=VAR 016599.
 FT T -> A (in allele Cw*0711).
 FT /FTID=VAR 016600.
 FT CG -> AA (IN REF. 8).
 FT R -> A (IN REF. 8).
 Query Match 2.6%; Score 8; DB 1; Length 366;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 249 VLWVLAVL 256
 DB 317 VLWVLAVL 324
 RESULT 6
 ID _IC18 HUMAN STANDARD; PRT; 366 AA.
 AC Q29865; O78203; P79498;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, Cw-18 alpha chain precursor
 DE (MHC class I antigen Cw*18).
 GN HLA-C OR HLA-C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (Cw*1801).
 RX MEDLINE=97161041; PubMed=9008313;
 RA Vilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreisler M.;
 RT "Molecular cloning of two new HLA-C alleles: Cw*1801 and Cw*0706.";
 RL Tissue Antigens 48:698-702(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (Cw*1801).
 RX MEDLINE=22512041; PubMed=12622774;
 RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
 RA Madrigal J.A., Little A.-M.;
 RT "Cloning and sequencing full-length HLA-B and -C genes.";
 RL Tissue Antigens 61:20-48(2003).

RN [3] SEQUENCE OF 26-206 FROM N.A. (Cw*1801).
 RP MEDLINE=98119594; PubMed=9459506;
 RA Grundschober C., Labonne M., Javaux F., Steiner Q.G., Gebuhrer L.,
 RA Tiercy J.M.;
 RT "Sequence of four new HLA-Cw alleles: a possible role of interallelic
 RT recombination.";
 RL Tissue Antigens 51:72-79(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (Cw*1802).
 RX MEDLINE=97378891; PubMed=92344488;
 RA Vilches C., Bunce M., de Pablo R., Moreno M.B., Puente S., Sanz L.,
 RA Kreisler M.;
 RT "The novel HLA-Cw*1802 allele is found associated with B*5703 in the
 RT Bubi population from Equatorial Guinea.";
 RL Tissue Antigens 49:644-649(1997).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- POLYMORPHISM: The following alleles of Cw-18 are known: Cw*1801
 CC (Cw*04GB) and Cw*1802 (Cw*18GB). The sequence shown is that of
 CC Cw*1801.
 CC -----
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 CC -----
 DR EMBL; X96582; CAA65401.1; -;
 DR EMBL; AJ420253; CAD12438.1; -;
 DR EMBL; Z80227; CAB02408.1; -;
 DR EMBL; Y09156; CAA70354.1; -;
 DR HSSP; P30460; IAGD.
 DR Genew; HGNC:4933; HLA-C.
 DR MIM; 142840; -;
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 KW SIGNAL 1 24
 FT CHAIN 25 366 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT CW-18 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 333
 FT DOMAIN 334 366 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
 FT VARIANT 319 319 V -> A (in allele Cw*1802).
 FT /FTID=VAR_016635.
 SQ SEQUENCE 366 AA; 40933 MW; 67CE7E948E4327D8 CRC64;
 Query Match 2.6%; Score 8; DB 1; Length 366;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 249 VLWVLAVL 256

Db 317 VLWVLAVL 324
 RESULT 7
 YGIK_SALTY
 ID YGIK_SALTY STANDARD; PRT; 435 AA.
 AC P40800;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein ygiK.
 GN YGIK OR SNG3171.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RA Cong J., Schmid M.B.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO THE YIAN/YGIK FAMILY.
 CC -----
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 CC -----
 DR EMBL; U09309; AAA56680.1; -;
 DR EMBL; AB008845; AAL22045.1; -;
 DR StyGene; SG10523; YGIK.
 DR InterPro; IPR000252; DedA.
 DR InterPro; IPR004681; TRAP_transptDctM.
 DR Pfam; PF00597; DedA; 1.
 DR TIGRFAMs; TIGR00786; dctM; 1.
 KW Hypothetical protein; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 57 77 POTENTIAL.
 FT TRANSMEM 110 130 POTENTIAL.
 FT TRANSMEM 146 166 POTENTIAL.
 FT TRANSMEM 176 196 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 280 300 POTENTIAL.
 FT TRANSMEM 321 341 POTENTIAL.
 FT TRANSMEM 343 363 POTENTIAL.
 FT TRANSMEM 367 387 POTENTIAL.
 FT TRANSMEM 408 428 POTENTIAL.
 FT TRANSMEM 119 119 A -> R (IN REF. 1).
 FT CONFLICT 124 124 A -> P (IN REF. 1).
 SQ SEQUENCE 435 AA; 46004 MW; BEA79EFCFE8A58A CRC64;
 Query Match 2.6%; Score 8; DB 1; Length 435;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CC EMBL; AF084561; AAD21808.1; -.
DR EMBL; AF084567; AAD21809.1; -.
DR EMBL; AF084562; AAD21809.1; JOINED.
DR EMBL; AF084563; AAD21809.1; JOINED.
DR EMBL; AF084564; AAD21809.1; JOINED.
DR EMBL; AF084565; AAD21809.1; JOINED.
DR EMBL; AF084566; AAD21809.1; JOINED.
DR EMBL; AF011381; CAA09601.1; -.
DR EMBL; BC046422; AAH46422.1; -.
DR HSP; P12259; 1CZT.
DR MGD; MGI:1336189; Relh.
DR InterPro; IPR000421; PA58 C.
DR InterPro; IPR008979; Gal_Bind_like.
DR Pfam; PF00754; F5_P8_type_C; 1.
DR SMART; SM00231; PA58C; 1.
DR PROSITE; PS01285; PA58C 1; 1.
DR PROSITE; PS01286; PA58C 2; FALSE_NEG.
DR PROSITE; PS00222; PA58C 3; 1.
KW Cell adhesion; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 224 RETINOSCHISIN.
FT DOMAIN 63 219 F5/8 TYPE C.
FT DISULFID 63 219 BY SIMILARITY.
SQ SEQUENCE 224 AA; 25575 MW; 4536203CC00E90E4 CRC64;
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Query Match 2.3%; Score 7; DB 1; Length 224;

Best Local Similarity 100.0%; Pred. No. 36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 FLLLLLP 24

Db 8 FLLLLLP 14

RESULT 10
RS2 SHEON

ID RS2 SHEON STANDARD; PRT; 242 AA.

AC Q8EGH5;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE 30S ribosomal protein S2.

GN RPSB OR S01629.

OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Alteromonadaceae; Shewanella.

OX NCBI_TaxID=70863;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MR-1;

RX MEDLINE=22297686; PubMed=12368813;

RA Heidelberg J.P., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

RA Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.P.,

RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,

RA Vamathevan J., Weidman J., Imbraim M., Lee K., Berry K., Lee C.,

RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

RA Feldblyum T.V., Smith H.O., Venter J.C., Nealeon K.H., Fraser C.M.;

RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

Shewanella oneidensis."

RL Nat. Biotechnol. 20:1118-1123(2002).

CC -1- SIMILARITY: Belongs to the S2P family of ribosomal proteins.

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CC EMBL; AE015609; AAN54684.1; -.
DR TIGR; S01629; -.
DR HAMAP; MF 00291; -. 1.
DR InterPro; IPR001865; Ribosomal S2.
DR InterPro; IPR005706; Ribosomal_S2_b/o.
DR Pfam; PF00318; Ribosomal_S2; 1.
DR PRINTS; PR00395; RIBOSOMALS2.
DR TIGRFAMs; TIGR01011; rpsB_bact; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 242 AA; 26569 MW; 74AA24550750B88C CRC64;

Query Match 2.3%; Score 7; DB 1; Length 242;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 288 PDGVNYI 294

Db 193 PDGVNYI 199

RESULT 11

TNFC_HUMAN

ID TNFC_HUMAN STANDARD; PRT; 244 AA.

AC Q06643; P78370; Q99761;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Lymphotoxin-beta (L1-beta) (Tumor necrosis factor C) (TNF-C) (Tumor

necrosis factor ligand superfamily member 3)).

GN LTB OR TNFSF3 OR TNFC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.

RC TISSUE=T-Cell;

RX MEDLINE=93208881; PubMed=7916655;

RA Browning J.L., Ngam-Ek A., Lawton P., Demarinis J., Tizard R.,

RA Chow E.P., Hession C., O'Brine-Greco B., Poley S.F., Ware C.F.;

RT "Lymphotoxin beta, a novel member of the TNF family that forms a

heteromeric complex with lymphotoxin on the cell surface."

RL Cell 72:847-856(1993).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RX MEDLINE=97445965; PubMed=9299492;

RA Warzocha K., Renard N., Charlot C., Bienvenu J., Coiffier B.,

RA Salles G.;

RT "Identification of two lymphotoxin beta isoforms expressed in human

lymphoid cell lines and non-Hodgkin's lymphomas."

RL Biochem. Biophys. Res. Commun. 238:273-276(1997).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=93208881; PubMed=7916655;

RA Neville M.J., Milner C.M., Campbell R.D.;

RT "A new member of the immunoglobulin superfamily and a V-ATPase G

subunit are amongst the predicted products of novel genes close to the

TNF locus in the human MHC."

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=97445965; PubMed=9299492;

RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

RA Abbas N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

RA Lasky S., Hood L.;

RT "Sequence of the human major histocompatibility complex class III

region."

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=97445965; PubMed=9299492;

RA Shih S., Tamiya G., Oka A., Inoko H.;

RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."

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```
CC EMBL; AB054536; BAB83881.1; --
CC EMBL; AB100082; BAC78156.1; --
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 19 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 49 244 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 222 222 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 244 AA; 25420 MW; A4047858335D5B97 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLAVLAL 258
Db 40 VLAVLAL 46

RESULT 13
ID HTPX AQUAE STANDARD; PRT; 302 AA.
AC O67798;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable protease htpx homolog (EC 3.4.24.-).
GN HTPX OR AQ 1991.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358(1998).
CC -|- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: Belongs to peptidase family M48.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE000766; AAC07747.1; --
DR PIR; B70471; B70471.
DR MEROPS; M48.004; --.
DR HAMAP; MF 00188; --.
DR InterPro; IPR006025; Pept_Mn_Zn_BS.
DR InterPro; IPR001915; Peptidase_M48.
DR Pfam; PF01435; Peptidase_M48; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
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```
KW Transmembrane; Hydrolase; Metalloprotease; Zinc; Complete proteome.
FT TRANSMEM 27 47 POTENTIAL.
FT TRANSMEM 151 171 POTENTIAL.
FT TRANSMEM 195 215 POTENTIAL.
FT METAL 141 141 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 142 142 BY SIMILARITY.
FT METAL 145 145 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 302 AA; 33030 MW; 3278BF481568895 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 IGGIIGG 248
Db 31 IGGIIGG 37

RESULT 14
ID TNFC MOUSE STANDARD; PRT; 306 AA.
AC P41155;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE necrosis factor ligand superfamily member 3).
GN LTB OR TNFSP3 OR TNFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=95148600; PubMed=7846035;
RA Pokholok D.K., Maroulakou I.G., Kuprash D.V., Alimzhanov M.B.,
RA Kozlov S.V., Novobrantseva T.I., Turetskaya R.L., Green J.E.,
RA Nedospasov S.A.;
RT "Cloning and expression analysis of the murine lymphotoxin beta
RT gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:674-678(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=9508371; PubMed=7995944;
RA Lawton P., Nelson J., Tizard R., Browning J.L.;
RT "Characterization of the mouse lymphotoxin-beta gene.";
RL J. Immunol. 154:239-246(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,
RA Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility class III region.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Cytokine that binds to LTB/TNFRSF3. May play a specific
CC role in immune response regulation. Provides the membrane anchor
CC for the attachment of the heterotrimeric complex to the cell
CC surface.
CC -|- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC (less prevalent) two LTA and one LTB subunits (By similarity).
CC -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -|- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
CC EMBL; U12029; AAA67716.1; --
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DR EMBL; U16984; AAB60493.1; -.
DR EMBL; U16985; AAA70089.1; -.
DR EMBL; U06950; AAA18592.1; -.
DR EMBL; AF109719; AAC82483.1; -.
DR PIR; I49139; I49139.
DR MGD; MGI:104786; Lcb.
DR GO; GO:0007515; Piliyoph gland development; IMP.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS00449; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
KW CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 27
FT TRANSMEM 28 48
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 49 306
FT EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 98 98
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 306 AA; 32328 MW; 87D276AB84A22549 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLAVLAL 258
DB 40 VLAVLAL 46

RESULT 15
TNFC_MARMO STANDARD; PRT; 310 AA.
ID TNFC_MARMO
AC Q9JMI0; Q9JMI1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE necrosis factor ligand superfamily member 3).
GN LTB OR TNFSF3 OR TNFC.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20184748; PubMed=10721723;
RA Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
RT "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
RT structure, characterization and biological activity.";
RL Gene 242:295-305(2000).
CC -!- FUNCTION: Cytokine that binds to LTR/TNFRSF3. May play a specific
CC role in immune response regulation. Provides the membrane anchor
CC for the attachment of the heterotrimeric complex to the cell
CC surface.
CC -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC (less prevalent) two LTA and one LTB subunits (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (potential).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC or send an email to license@isb-sib.ch).
```

```
CC EMBL; AF096268; AAF34866.1; -.
DR EMBL; AF095587; AAF34865.1; -.
DR HSSP; P01374; 1TNR.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS00449; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
KW CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 27
FT TRANSMEM 28 48
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 49 310
FT EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 272 272
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 280 280
FT D -> H (IN REF. 1; AAF34865).
SQ SEQUENCE 310 AA; 32644 MW; 73B354EFC8B3B3BE CRC64;

Query Match 2.3%; Score 7; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLAVLAL 258
DB 40 VLAVLAL 46
```

Search completed: June 15, 2004, 11:10:31
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: June 15, 2004, 11:05:50 ; Search time 36 Seconds
(without alignments)
2716.962 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPRLRLCARLPDFL.....VNYITDEGDFRHKSPVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mbc.*
- 8: sp_organalle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertibrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	4 Q9BX67	Q9bx67 homo sapien
2	310	100.0	355	4 Q8WVL8	Q8wvl8 homo sapien
3	208	67.1	309	4 Q96FL1	Q96fl1 homo sapien
4	32	10.3	310	11 Q9D8B7	Q9d8b7 mus musculus
5	28	9.0	310	11 Q9D1M9	Q9d1m9 mus musculus
6	28	9.0	310	11 Q9EPK4	Q9epk4 mus musculus
7	13	4.2	64	11 Q8BT59	Q8bt59 mus musculus
8	8	2.6	39	7 Q9TNT2	Q9tnt2 homo sapien
9	8	2.6	67	7 Q8HWG1	Q8hwg1 homo sapien
10	8	2.6	76	5 Q857W1	Q857w1 procamburus
11	8	2.6	131	5 Q818S1	Q818s1 anopheles 9
12	8	2.6	154	11 Q8CAV2	Q8cav2 mus musculus
13	8	2.6	231	16 Q89E35	Q89e35 bradyrhizob
14	8	2.6	231	17 Q9TQ75	Q8tqt5 methanosarc
15	8	2.6	232	17 Q8ZSR8	Q8zar8 pyrobaculum
16	8	2.6	233	10 Q9LR49	Q9lr49 arabidopsis

17	8	2.6	246	5 Q966C0	Q966c0 caenorhabdi
18	8	2.6	294	16 Q98EQ9	Q98eq9 rhizobium 1
19	8	2.6	309	5 Q9N4Y9	Q9ny9 caenorhabdi
20	8	2.6	322	2 Q9RPI7	Q9rpi7 desulfitoba
21	8	2.6	336	10 Q9C7E9	Q9c7e9 arabidopsis
22	8	2.6	338	7 Q9MXL5	Q9mxl5 pan troglod
23	8	2.6	348	7 Q9MWJ9	Q9mwj9 gorilla gor
24	8	2.6	348	16 Q9PR46	Q9pr46 ureaplasma
25	8	2.6	363	7 Q95HC2	Q95hc2 homo sapien
26	8	2.6	365	7 Q9XRK8	Q9xrk8 pongo pygma
27	8	2.6	365	7 Q9XRK7	Q9xrk7 pongo pygma
28	8	2.6	365	7 Q9MXG4	Q9mxg4 pan troglod
29	8	2.6	366	6 Q46684	Q46684 pan troglod
30	8	2.6	366	7 Q8MHO0	Q8mho0 pongo pygma
31	8	2.6	366	7 Q8MHI1	Q8mhi1 pongo pygma
32	8	2.6	366	7 Q8MHG8	Q8mhg8 pongo pygma
33	8	2.6	366	7 Q8MHG9	Q8mhg9 pongo pygma
34	8	2.6	366	7 Q19617	Q19617 homo sapien
35	8	2.6	366	7 Q860B0	Q860b0 homo sapien
36	8	2.6	366	7 Q85ZX8	Q85zx8 homo sapien
37	8	2.6	366	7 Q9TPL2	Q9tpl2 pan troglod
38	8	2.6	366	7 Q9MKD2	Q9mkd2 pan troglod
39	8	2.6	366	7 Q7YQB2	Q7yqb2 homo sapien
40	8	2.6	449	16 Q8CWZ7	Q8cwz7 streptococc
41	8	2.6	452	16 Q8G5D2	Q8g5d2 bifidobacte
42	8	2.6	492	16 Q8Z1U9	Q8z1u9 salmonella
43	8	2.6	659	16 Q8EK37	Q8ek37 shewanella
44	8	2.6	784	16 Q9CIF4	Q9cif4 lactococcus
45	8	2.6	1290	13 Q9W6E1	Q9w6e1 gallus gall

ALIGNMENTS

RESULT 1

Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein FLJ90828).
DE FLJ90288) (Hypothetical protein FLJ90828).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3."; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Aurand-Lions M.A., Johnson-leger C., Wong C., Dupasquier L.;
RT "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members."; Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Aurand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial junctions."; Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT "Characterization of Junctional Adhesion Molecule-3 on Human Platelets: A New Member of Immunoglobulin Superfamily.";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

[5]
RN SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Iehi S., Kawai-Hio Y., Saito K.,
RA Yamanoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Iotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NEO human cDNA sequencing project";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF356518; AK27221.1; -;
DR EMBL; AJ344431; CAC69845.1; -;
DR EMBL; AF448478; AM20925.1; -;
DR EMBL; AK074769; BAC11195.1; -;
DR EMBL; AK075309; BAC11538.1; -;
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Hypothetical protein; Signal. POTENTIAL.
FT SIGNAL 1 30
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EADAB9 CRC64;

Query Match 100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRPVVOBFESVELSCIITDSQT 60
DB 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRPVVOBFESVELSCIITDSQT 60
QY 61 SDPIEWKKIQDEQTYVPFDNKKIQGLAGRAEILGKTSIKIWNVTRDSALYRCEVVAR 120
DB 61 SDPIEWKKIQDEQTYVPFDNKKIQGLAGRAEILGKTSIKIWNVTRDSALYRCEVVAR 120
QY 121 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRFRNSSPHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEVYDL 240
DB 181 PTDSRANPRFRNSSPHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEVYDL 240
QY 241 NTGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQGESYKPKPGDGVNVRTDESG 300
DB 241 NTGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQGESYKPKPGDGVNVRTDESG 300
QY 301 DFRHKSSFVI 310
DB 301 DFRHKSSFVI 310

RESULT 2

Q8WML8
ID Q8WML8 PRELIMINARY; PRT; 355 AA.
AC Q8WML8
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junction adhesion molecule 3.
GN JAM3
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hearn T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Phillips H.M.;
RT "Narrowing the critical region within 11q24-quer for hypoplastic left
RT heart and identification of a candidate gene, JAM3, expressed during

RT cardiogenesis";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416101; CAC94776.1; -;
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Immunoglobulin domain.
FT CHAIN 76 355
SQ SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

Query Match 100.0%; Score 310; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRPVVOBFESVELSCIITDSQT 60
DB 46 MALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRPVVOBFESVELSCIITDSQT 105
QY 61 SDPIEWKKIQDEQTYVPFDNKKIQGLAGRAEILGKTSIKIWNVTRDSALYRCEVVAR 120
DB 106 SDPIEWKKIQDEQTYVPFDNKKIQGLAGRAEILGKTSIKIWNVTRDSALYRCEVVAR 165
QY 121 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 166 NDRKEIDEIVELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 225
QY 181 PTDSRANPRFRNSSPHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEVYDL 240
DB 226 PTDSRANPRFRNSSPHLNSETGLVFTAVHKDDSGQYCIASNDAGSARCEQEMEVYDL 285
QY 241 NTGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQGESYKPKPGDGVNVRTDESG 300
DB 286 NTGGIIGGVLVAVLALITLIGCCAYRRGYFINNKQGESYKPKPGDGVNVRTDESG 345
QY 301 DFRHKSSFVI 310
DB 346 DFRHKSSFVI 355

RESULT 3

Q96FL1
ID Q96FL1 PRELIMINARY; PRT; 309 AA.
AC Q96FL1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010690; AAH10690.1; -;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
FT NON TER 1
SQ SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;

Query Match 67.1%; Score 208; DB 4; Length 309;
Best Local Similarity 99.7%; Pred. No. 7.5e-212;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 ALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTFVQBFESVLSLSCIITDSQTS 61
DB 1 ALRRPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTFVQBFESVLSLSCIITDSQTS 60
QY 62 DPRIEWKIOBQTTYYVFFDNKIQGLDLAGRAELIGKTSKIMVNRDSDALYRCEVVARN 121
DB 61 DPRIEWKIOBQTTYYVFFDNKIQGLDLAGRAELIGKTSKIMVNRDSDALYRCEVVARN 120
QY 122 DRKEIDIEIVLTIVQVKPVTVCVRPKAVPVGKMATLHCQESGHPHYSWYRNDVPLP 181
DB 121 DRKEIDIEIVLTIVQVKPVTVCVRPKAVPVGKMATLHCQESGHPHYSWYRNDVPLP 180
QY 182 TDSRANPRFNSSPHLNSGTGLVTAHVHDSGQYCIASNDAGSARCEQEVEYDLN 241
DB 181 TDSRANPRFNSSPHLNSGTGLVTAHVHDSGQYCIASNDAGSARCEQEVEYDLN 240
QY 242 IGGIIGVVLVLAVALITIGICCAVYRGYFINKQDGSYKPGKPDGVNYIRTDDEGD 301
DB 241 IGGIIGVVLVLAVALITIGICCAVYRGYFINKQDGSYKPGKPDGVNYIRTDDEGD 300
QY 302 FRHKSSPVI 310
DB 301 FRHKSSPVI 309

RESULT 4
Q9DB87 ID Q9DB87 PRELIMINARY; PRT; 310 AA.
AC Q9DB87;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKS; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74894EABE234680 CRC64;

Query Match 10.3%; Score 32; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 EFESVLSLSCIITDSQTSDPRIEWKIQD 72
DB 45 EFESVLSLSCIITDSQTSDPRIEWKIQD 72

RESULT 6
Q9BPK4 ID Q9BPK4 PRELIMINARY; PRT; 310 AA.
AC Q9BPK4;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKS; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74894EABE234680 CRC64;

Query Match 10.3%; Score 32; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PVQEFESVLSLSCIITDSQTSDPRIEWKIQD 72
DB 41 PVQEFESVLSLSCIITDSQTSDPRIEWKIQD 72

RESULT 5
Q9D1M9 ID Q9D1M9 PRELIMINARY; PRT; 310 AA.
AC Q9D1M9;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKS; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 9.0%; Score 28; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 EFESVLSLSCIITDSQTSDPRIEWKIQD 72
DB 45 EFESVLSLSCIITDSQTSDPRIEWKIQD 72

RESULT 6
Q9BPK4 ID Q9BPK4 PRELIMINARY; PRT; 310 AA.
AC Q9BPK4;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKS; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 9.0%; Score 28; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RT Auranf-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AJ300304; CAC20704.1; -.
DR EMBL; AK013156; BAB28683.1; -.
DR EMBL; BC024357; AAH24357.1; -.
DR EMBL; AK032833; BAC28049.1; -.
DR MGD; MGI:193825; Jam3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;

Query Match 9.0%; Score 28; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 9.5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 EFESVELSCIITDTSQSDPRIENKKIQD 72
DB |||||||||||||||||||||||||||
45 EFESVELSCIITDTSQSDPRIENKKIQD 72

RESULT 7
Q8BT59 PRELIMINARY; PRT; 64 AA.
ID Q8BT59
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AC Q8BT59;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Junction cell adhesion molecule 3 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK017692; BAC25526.1; -.
DR NON_TER 1
SQ SEQUENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;

Query Match 4.2%; Score 13; DB 11; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 EEGDFRHKSSPVI 310
DB |||||||||||||||
52 EEGDFRHKSSPVI 64

RESULT 8
Q8TNT2 PRELIMINARY; PRT; 39 AA.
ID Q8TNT2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MHC class I HLA C antigen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=99110146; PubMed=9894855;
RA van der Vlies S., Voorter C., van den Berg-Loonen B.;
RT "A reliable and efficient high resolution typing method for HLA C
RT using sequence-based typing.";
RL Tissue Antigens 52:558-568(1998).
DR EMBL; Y16418; CAA76206.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 3938 MW; 24613855AD783823 CRC64;

Query Match 2.6%; Score 8; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 VLVVLAVL 256
DB |||||||
18 VLVVLAVL 25

RESULT 9
Q8HWG1 PRELIMINARY; PRT; 67 AA.
ID Q8HWG1
AC Q8HWG1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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DE MHC class I antigen (Fragment).
GN HLA-CW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-17 FROM N.A.
RA Delfino L., Morabito A., Ferrara G.B.;
RT "HLA-Cw*07012 sequence updating: from exon 6 to exon 8";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY162385; AAN84536.1; -.
DR EMBL; AY162382; AAN84536.1; JOINED.
DR EMBL; AY162383; AAN84536.1; JOINED.
DR EMBL; AY162384; AAN84536.1; JOINED.
FT NON TER 1
SQ SEQUENCE 67 AA; 6538 MW; 543B57F5P97D7PF1 CRC64;

Query Match 2.6%; Score 8; DB 7; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
Db 18 VLVVLAVL 25

RESULT 10
Q867W1 PRELIMINARY; PRT; 76 AA.
AC Q867W1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide precursor protein.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Cambaridae; Procamburus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasuda-Kamatani Y., Yasuda A.;
RT "Cloning of cDNA for a neuropeptide precursor protein from Procamburus clarkii";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036712; BAC55939.1; -.
DR EMBL; AB036713; BAC55940.1; -.
SQ SEQUENCE 76 AA; 7895 MW; 3A3DF225947483AA CRC64;

Query Match 2.6%; Score 8; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
Db 14 VLVVLAVL 21

RESULT 11
Q818S1 PRELIMINARY; PRT; 131 AA.
AC Q818S1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Odorant-binding protein G.388.a.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.

RA Xu P., Smith D.P.;
RT "Identification of distinct families of odorant-binding in the genome of Anopheles gambiae";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY146730; AAO12090.1; -.
DR GO; GO:0005549; F:Odorant binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006170; PBP GOBP.
DR Pfam; PF01395; PBP GOBP; 1.
SQ SEQUENCE 131 AA; 14884 MW; FC7D52E9740E2A64 CRC64;

Query Match 2.6%; Score 8; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 IGGVLVVL 253
Db 7 IGGVLVVL 14

RESULT 12
Q8C4V2 PRELIMINARY; PRT; 154 AA.
AC Q8C4V2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSU=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK080981; BAC38104.1; -.
KW Hypothetical protein.
SQ SEQUENCE 154 AA; 17098 MW; F032A4B8C5483EC6 CRC64;

Query Match 2.6%; Score 8; DB 11; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 DAGSARCE 231
Db 72 DAGSARCE 79

RESULT 13
Q89E35 PRELIMINARY; PRT; 231 AA.
AC Q89E35;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BL17252 protein.
GN BL17252.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,

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RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005961; BAC52517.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004254; HlyIII-related.
DR Pfam; PF03006; UPP0073; 1.
KW Complete proteome.
SQ SEQUENCE 231 AA; 25052 MW; 254BB5B98D40D58B CRC64;

Query Match 2.6%; Score 8; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 LVVLAVL 256
DB 50 LVVLAVL 57
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RESULT 14
Q8TQTS PRELIMINARY; PRT; 231 AA.
AC Q8TQTS;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cell surface lipoprotein.
GN MA1454.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010815; AAM04868.1; -.
DR InterPro; IPR008972; Cupredoxin.
KW Lipoprotein; Complete proteome.
SQ SEQUENCE 231 AA; 25437 MW; 7AAB21CEE0B6500B CRC64;

Query Match 2.6%; Score 8; DB 17; Length 231;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVLA 257
DB 23 LVVLAVLA 30
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RESULT 15
Q8ZSR8 PRELIMINARY; PRT; 232 AA.
AC Q8ZSR8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Hypothetical protein PAE3614.
GN PAE3614.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009941; AAL65045.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 232 AA; 25942 MW; 39A5B8CC403F903 CRC64;

Query Match 2.6%; Score 8; DB 17; Length 232;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 DFFLLLLF 24
DB 2 DFFLLLLF 9
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Search completed: June 15, 2004, 11:11:56
Job time : 37 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2004, 11:01:19 ; Search time 16.5 Seconds
(without alignments)
969.942 Million cell updates/sec

Title: US-09-524-531c-15

Perfect score: 1637

Sequence: 1 MALRRPRLRLCARLPDFL.....VNVIRDEGDFRHKSFVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgm2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/2/iaa/PCrUS_COMB.pep.*
6: /cgm2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1637	100.0	310	4	US-09-907-794A-423
2	1637	100.0	310	4	US-09-905-125A-423
3	1637	100.0	310	4	US-09-902-775A-423
4	481	29.4	298	4	US-09-152-060-76
5	461.5	28.2	312	4	US-09-254-465A-9
6	461.5	28.2	312	4	US-09-907-794A-64
7	461.5	28.2	312	4	US-09-905-125A-64
8	461.5	28.2	312	4	US-09-902-775A-64
9	457.5	27.9	300	4	US-09-254-465A-10
10	424	25.9	299	3	US-09-188-930-331
11	424	25.9	299	4	US-09-462-270-2
12	424	25.9	299	4	US-09-254-465A-1
13	424	25.9	299	4	US-09-312-283C-189
14	424	25.9	299	4	US-09-312-283C-331
15	424	25.9	299	4	US-09-907-794A-119
16	424	25.9	299	4	US-09-905-125A-119
17	424	25.9	299	4	US-09-902-775A-119
18	412	25.2	299	3	US-09-188-930-189
19	392.5	24.0	260	4	US-09-254-465A-23
20	392.5	24.0	263	4	US-09-254-465A-25
21	288	17.6	205	4	US-09-462-270-4
22	228.5	14.0	319	1	US-08-597-495B-22
23	228.5	14.0	319	3	US-09-068-051A-22
24	228.5	14.0	319	4	US-09-336-536-67
25	228.5	14.0	319	4	US-09-254-465A-6
26	217.5	13.3	270	4	US-09-254-465A-24
27	217.5	13.3	273	4	US-09-254-465A-26

28	215.5	13.2	318	3	US-09-068-051A-32
29	197.5	12.1	387	4	US-09-175-928-2
30	173.5	10.6	370	4	US-09-336-536-28
31	171.5	10.5	394	4	US-09-336-536-39
32	169.5	10.4	390	2	US-08-979-424-1
33	169.5	10.4	390	4	US-09-907-794A-39
34	169.5	10.4	390	4	US-09-905-125A-39
35	169.5	10.4	390	4	US-09-902-775A-39
36	167	10.2	365	4	US-09-336-536-40
37	166.5	10.2	341	4	US-09-336-536-29
38	163.5	10.0	398	4	US-09-778-510-6
39	163.5	10.0	398	4	US-09-907-794A-84
40	163.5	10.0	398	4	US-09-905-125A-84
41	163.5	10.0	398	4	US-09-902-775A-84
42	162.5	9.9	246	4	US-09-336-536-31
43	161	9.8	313	4	US-09-700-397-4
44	161	9.8	344	4	US-09-700-397-3
45	160.5	9.8	365	3	US-08-928-383B-2

ALIGNMENTS

RESULT 1

US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
US-09-507-794A-423

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Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SDPRIEWKKIQDEQTTVFPFDNKIQGLAGRAELTGKTSLKINWTRDSALYRCVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGKMATLHCQSESGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGKMATLHCQSESGHPRPHYSWYRNDVPL 180
QY 181 PTDSRANPRNSSFHNSGTGLVTAHVHDKDSGOYCIASNDAGSARCEQMEVYDL 240
DB 181 PTDSRANPRNSSFHNSGTGLVTAHVHDKDSGOYCIASNDAGSARCEQMEVYDL 240
QY 241 NIGGIIGGVVLAVLALITLIGICCAVRGYPINNKGDSYKNGKPGDGVNYIRTDERG 300
DB 241 NIGGIIGGVVLAVLALITLIGICCAVRGYPINNKGDSYKNGKPGDGVNYIRTDERG 300
QY 301 DFRHKSFFVI 310
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RESULT 2

US-09-905-125A-423
Sequence 423, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.

Query Match 100.0%; Score 1637; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 SDPRIEWKKIQDEQTTVFPFDNKIQGLAGRAELTGKTSLKINWTRDSALYRCVVAR 120
DB 61 SDPRIEWKKIQDEQTTVFPFDNKIQGLAGRAELTGKTSLKINWTRDSALYRCVVAR 120
QY 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGKMATLHCQSESGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVIELTVQVKPTVPCRVKAPVPGKMATLHCQSESGHPRPHYSWYRNDVPL 180